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Perfect score
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Gapop 10.0 , Gapext 0.5
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1: geneseqp19808:*
2: geneseqp19908:*
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MKKKKLEHHHHHHTSAGITK.....TTMRTSSAWRHPQFGGKKKK 334
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geneseqD2001s:*
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geneseqD2004s:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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ABG30587
ABG30597
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ABG32181
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HCPpatitis
Hepatitis
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ALIGNMENTS

HCV protease NS2/3 truncation 4K-6H (904-1206)st-4K.

05-NOV-2002

(first entry)

ABG32182;

ABG32182 standard; protein; 334 AA.

RESULT 1 ABG321182 ABG321182 ABG32183 AC ABG3 WPI; 2002-599511/64. N-PSDB; ABK90407. 15-DEC-2000; 2000US-0256031P. Peptide HCV; enzyme; protease; NS2/3 (810-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiniflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; 4K-6H (904-1206)st-4K; mutant; mutein. 13-DEC-2001; 2001WO-CA001796 20-JUN-2002. WO200248375-A2. Peptide Protein Synthetic. Thibeault D, Hepatitis C virus (BOEH) BOEHRINGER INGELHEIM CANADA LTD Lamarre D, /note= "Truncated NS2/3 protease" 319. .334 /note= Location/Qualifiers .302 .334 "4-Lys/His tag" "Streptavidin/4-Lys tag" Maurice R, Pilote Ļ

Claim 39; Fig 9B; 67pp; English

The invention

relates to an isolated polypeptide consisting

ō, ω

Novel polypeptide for screening inhibitors of non-structural useful as therapeutic agents against hepatitis C virus, complength non-structural protease, or its truncation.

tural proteases comprises full

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CC NS2/3 protease. Also included are (1) a composition (2) comprising an included are (1) a composition (2) comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) comprising as ABG32198; (3) protease; (2) a NS2/3 inhibitory peptide appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 chaotropic agent, refolding the protease in the presence of a reducing agent, and LDAO in the presence of reduced concentration of the chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 protease; (5) measuring (M3) the auto-cleavage active NS2/3 protease in a medium containing an activation detergent to induce auto-cleavage of the NS2/3 protease; (5) measuring (M3) the auto-cleavage activity of NS2/3 containing an incubating the active NS2/3 protease and produce containing a products or their fragments, and measuring the produced by M2 for sufficient time to induce auto-cleavage of NS2/3 protease and produce contained to incleaved NS2/3 protease produced by M2 for and (6) screening a potential inhibitor of auto-cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of contained to incleavage products or their fragments. The protease is contained to the protential inhibitor of auto-cleavage activity of an active NS2/3 protease, cleavage products or their fragments. The protease is contained to the development of in vitro assays for screening novel inhibitors of uncleaved in contained the development of in vitro assays for screening novel inhibitors of uncleaved contained the development of the information dependence of contained the protease is contained to the development of the contained the protease. The protease is contained the protease is contained to the protease of contained 
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Sequence 334 AA;
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δ B Ś 밁 Ś Ś В 8 맑 멅 181 301 241 181 121 121 241 334; 61 61 ь ы MKKKKLEHHHHHTSAGITKVÞYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTY EILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQS DLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRG FLATCYNGVCWTVFHGAGSKTLAGPKGPITOMYTNVDQDLVGWQAPPGARSMTPCTCGSS VYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGR VYDHLTPLODWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGR MKKKKLEHHHHHTSAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTY VAKAVDFIPVESMETTMRTSSAWRHPQFGGKKKK 334 DLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRG EILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQS FLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSS Conservative 0, Score 1771; DB 5; Pred. No. 5.4e-164; ; Mismatches 0; Indels 0 Gaps 300 300 240 240 180 120 120 60 0

Query Match Best Local

Similarity

100.0%;

Length

334;

RESULT 2
ABG32181
ID ABG3
XX
AC ABG:
XX
DT 05-ABG32181 standard; protein; 409 AA

301

VAKAVDFIPVESMETTMRTSSAWRHPQFGGKKKK

05-NOV-2002

(first entry)

HCV; enzyme; protease; NS2/3 (810-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; Synthetic Hepatitis C virus chaotropic agent; mutant; mutein.

HCV protease NS2/3 (810-1206).

Peptide Location/Qualifiers 398. .409. /note= "Streptavidin tag"

WO200248375-A2

20-JUN-2002

13-DEC-2001; 2001WO-CA001796

15-DEC-2000; 2000US-0256031P

(BOEH) BOEHRINGER INGELHEIM CANADA LTD.

Ď Lamarre ū Maurice R, Pilote L, Pause

WPI; 2002-599511/64. N-PSDB; ABK90406.

Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.

Claim 42; Fig 1B; 67pp; English.

The invention relates to an isolated polypeptide consisting of a fullcomparison of the potentials C virus) non-structural (NS)2/3 procease (referred CC length HCV (hepatitis C virus) non-structural (NS)2/3 procease (referred CC comparison of the potential CC residue amino acid 810 to 906, or having a minimal amino acid sequence CC from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC (NS2/3) protease. Also included are (1) a composition (comprising a sufficient concentration of lauryldiathylamine oxide (LDAO) CC comprising as ABG32198; (3) protease in the protease is in a solution of comprising as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 protease, involving isolating the protease in the presence of a gretucing agent, refolding the isolated protease by contacting it with a creducing agent, and LDAO in the presence of reduced concentration of the protease, involving inclustring refolded inactive NS2/3 protease, involving inclustring the auto-cleavage of the NS2/3 protease in a medium containing an activation detergent to induce auto-cleavage of NS2/3 protease, involving inclustring the active NS2/3 protease and produce Coleavage products or their fragments, and measuring the presence of the NS2/3 protease, involving inclustring the active NS2/3 protease and produce Cleavage products or their fragments, and measuring the presence of the potential inhibitor, comparing the amount of uncleaved contactivity of an containing the potential inhibitor, comparing the amount of uncleaved in cleavage products or their fragments. The presence of the development of in vitro assays for screening novel inhibitors of an contactive NS2/3 protease with contact characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of confidence of the screen of the s streptavividin

Sequence 409

Query Match Best Local Similarity 93.7%; 100.0%; Score 1660; DB 5; Pred. No. 4.9e-153; Length 409

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RESULT 3
ABG32183
ID ABG3
ID ABG3
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AC ABG3
XX
DT 05-N
XX
Chack
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The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal residue amino acid 810 to 906, or having a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV).1b-40 full-length NS2/3 protease. Also included are (1) a composition (C) comprising an isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a murated sequence, where the protease is in a solution
                                                                                                                                                                                                                                                                                                                  Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCV; enzyme; protease; NS2/3 (904-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
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                                                                                                                                                                                                                                                                  Page 58-59; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide capearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 protease, involving isolating the protease in the presence of a CC chaotropic agent, and LDAO in the presence of reduced concentration of the chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 CC protease, involving diluting refolded inactive NS2/3 protease in a medium CC containing an activation detergent to induce auto-cleavage of the NS2/3 protease; (5) measuring (M3) the auto-cleavage activity of NS2/3 CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3 CC protease; involving incubating the active NS2/3 protease and produce containing an incubating the auto-cleavage of NS2/3 protease and produce contained the to induce auto-cleavage of NS2/3 protease and produce contained to incleaved NS2/3 protease, involving aprotease, cleavage products or their fragments, and measuring the presence or cc absence of uncleaved NS2/3 protease, cleavage products or their fragments; and measuring the presence of, or active NS2/3 protease, involving carrying out M3 in the presence of, or capsell for detailed blochemical inhibitor, comparing the amount of uncleaved NS2/3 protease, cleavage products or their fragments. The protease is useful for other contained the contained conta
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Best Local Similarity 100.
Matches 303; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide
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                                                                RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                     GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                                                                                                                 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET 315
                                                                                                                                                                          GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
             318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%; Score 1589; DB 5; 100.0%; Pred. No. 2.7e-146;
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ACA
                                     05-NOV-2002
                                                     ABG32187
                            protease NS2/3 truncation mutant 866-1206
                                                     standard; protein;
                                     entry)
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TINE R

HCV; enzyme; pr chronic liver d hepatotropic; a chaotropic ager agent; protease; NS2/3 (866-1206); hepatitis C virus infection; r disease; cirrhosis; end-stage liver disease; virucide; antiinflammatory; lauryldiethylamine oxide; LDAO; mutant; mutein

Hepatitis C virus.

20-JUN-2002 Synthetic. WO200248375-A2

13-DEC-2001; 2001WO-CA001796

15-DEC-2000; 2000US-0256031P

(BOEH) BOEHRINGER INGELHEIM CANADA LTD.

Thibeault D, Lamarre Maurice R, Pilote L, Pause

Novel polypeptide for as therapeutic non-structural screening inhibitors of non-structural proteases agents against hepatitis C virus, comprises full protease, or its truncation.

Claim 41; Page 62-63; 67pp; English.

CC residue amino acid 810 to 906, or having a minimal amino acid sequence CC from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC NS2/3 protease. Also included are (1) a composition (c) comprising an CC isolated HCV NS2/3 protease selected from full length NS2/3 protease, or CC its truncation or a mutated sequence, where the protease is in a solution CC comprising a sufficient concentration of lauryldisthylamine oxide (LDAO) CC to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 protease, involving isolating the protease in the presence of a CC chaotropic agent, refolding the isolated protease by contacting it with a CC chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 protease, involving diluting refolded inactive NS2/3 protease in a medium CC containing an activation detergent to induce auto-cleavage of the NS2/3 CC protease, involving incubating the active NS2/3 protease in a medium CC containing an activation detergent to induce auto-cleavage of the NS2/3 CC protease, involving incubating the active NS2/3 protease activity of NS2/3 CC protease, involving incubating the active NS2/3 protease produced by M2 CC for sufficient time to induce auto-cleavage products or their fragments, and measuring the presence of cc laevage products or their fragments, and measuring the presence of cc absence of the potential inhibitor, comparing the amount of uncleaved CC useful for detailed biochemical characterisation of the enzymes and in the pritro account of uncleaved is cuseful for detailed biochemical characterisation of the enzymes and in the protease is the development of in vitro assays for screening novel inhibitors of NS2/3 protease which are useful as therapeutic agents against HCV infection (which causes chronic liver disease, cirrhosis and end-stage liver disease. Mis useful for high level production of protease. The present sequence represents the NS2/3 truncation mutant 866-1206 (numbered relative to the full length NS2/3 protein) length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal to an isolated polypeptide consisting of a C virus) non-structural (NS) 2/3 protease (1

Sequence 341 AA;

Query Match Best Local :

Similarity

89.7%; 100.0%;

Score 1589; DB 5; Pred. No. 3.2e-146;

Length 341;

당 밁 Ş 멅 Ş Š Matches Local Sim thes 303; 16 99 76 υ e AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG <u>LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW</u> Conservative <u>,</u> Mismatches Indels 0 218 195 158 98

ABG32186
ID ABG321 Ś Ş 밁 В S HCV; enzyme; protease; NS2/3 (855-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; 05-NOV-2002 Thibeault D, 15-DEC-2000; 13-DEC-2001; 2001WO-CA001796 20-JUN-2002 WO200248375-A2 Synthetic Hepatitis C virus. chaotropic agent; mutant; mutein. HCV protease ABG32186; ABG32186 (BOEH) BOEHRINGER INGELHEIM CANADA LTD .196 316 279 256 219 TMR standard; RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 2000US-0256031P 318 NS2/3 truncation mutant 855-1206. (first entry) protein; Maurice R, Pilote L, 338 315 278

Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.

Claim 41; Page 61-62; 67pp; English.

The invention relates to an isolated polypeptide consisting of a fullCC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC (NS2/3 protease. Also included are (1) a composition (C) comprising an CC its truncation or a mutated sequence, where the protease is in a solution CC comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) CC comprising as ABG32198, (3) producing (M1) a refolded, inactive HCV NS2/3 concentration of lauryldiethylamine oxide (LDAO) CC chaotropic agent, refolding the protease in the presence of a concentration of the protease, involving isolating the protease in the presence of a containing agent, and LDAO in the presence of reduced concentration of the containing an activation detergent to induce auto-cleavage of the NS2/3 protease, involving includating the isolated protease by contacting it with a containing an activation detergent to induce auto-cleavage of the NS2/3 protease, involving incubating the active NS2/3 protease in a medium containing an activation detergent to induce auto-cleavage of the NS2/3 protease, involving incubating the active NS2/3 protease and produce colleavage producets or their fragments, and measuring the presence or cleavage producet or their fragments, and measuring the presence or

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KW Chrc
KW Chac
XX Chac
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DE Ş 밁 Ş B Ş 片 5 B Š 멂 á Query Match Best Local (Matches absence of uncleaved NS2/3 protease, cleavage products or their fragments, and (6) screening a potential inhibitor of auto-cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of, or absence of the potential inhibitor, comparing the amount of uncleaved NS2/3 protease, cleavage products or their fragments. The protease is useful for detailed biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of NS2/3 protease which are useful as therapeutic agents against HCV infection (which causes chronic liver disease, cirrhosis and end-stage liver disease. M1 is useful for high level production of protease. The present sequence represents the NS2/3 truncation mutant 855-1206 (numbered relative to the full length NS2/3 protein) HCV; enzyme; protease; NS2/3 (827-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein. ACA Hepatitis C Synthetic. 05-NOV-2002 ABG32185 Sequence 352 13-DEC-2001; 15-DEC-2000; 2000US-0256031P. (BOEH) BOEHRINGER INGELHEIM CANADA LTD. protease 170 110 303; 316 290 230 196 136 350 50 76 16 Similarity TAN THE GAGSKTLAGPKGPITOMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH standard; protein; 380 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAXAVDFIFVESMET RILAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH Ħ RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR Conservative AA; virus 318 2001WO-CA001796 NS2/3 truncation mutant 827-1206 352 (first entry) 89.7%; 100.0%; Score 1589; DB 5; ; Pred. No. 3.4e-146; 0 Mismatches 0 Length Indels 0 315 135 75 349 255 195 169 109 289 229

length polypeptide for screening inhibitors of non-structural l as therapeutic agents against hepatitis C virus, components truncation.

Claim 41; Page 60-61; 67pp; English.

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Ingth HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred CC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence (from residues 904 to 1206 of hepatitis C virus (HCV) 11-40 full-length CC (NS2/3) protease. Also included are (1) a composition (c) comprising a sufficient concentration of lauryldathylamine oxide (LDAO) CC to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide cappearing as ABG32198; (3) produces in the presence of a chaotropic agent, refolding the isolated protease by contacting it with a CC reducing agent, and LDAO in the presence of reduced concentration of the concentration of the concentration of the concentration of the protease; (1) an active NS2/3 protease; involving diluting refolded inactive (NS2/3) are cleave; (1) measuring (M3) the auto-cleavage activity of NS2/3 protease; (2) an activation detergent to induce auto-cleavage of the NS2/3 protease; (3) measuring (M3) the auto-cleavage activity of NS2/3 protease; (3) measuring (M3) the active NS2/3 protease and produce cleavage products or their fragments, and measuring the presence of a absence of uncleaved NS2/3 protease, cleavage products or their fragments, and measuring the presence of, and (6) screening a potential inhibitor of auto-cleavage activity of an active NS2/3 protease; cleavage products or their fragments or their fragments of the protease is considered to induce auto-cleavage activity of an active NS2/3 protease is protease. Involving carrying out M3 in the presence of, or cative NS2/3 protease, cleavage products or their fragments. The protease is considered to involve active notation of the enzymes and in the development of in vitro assays for screening novel inhibitors of constant the constant the novel protease. The protease, the full length NS2/3 protease. The protease of the protease which are useful for high leve

Sequence 380 AA;

Length 380;

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Best Local
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                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                    LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW
                                                     RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                             RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGI
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        318
                                                                                                                                                                                                                                                                                                    89.7%; Score 1589; DB 5; 100.0%; Pred. No. 3.8e-146;
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Thibeault

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Lamarre

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Maurice R,

Pilote

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The invention relates to an isolated polypeptide consisting of a full-
CC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred
CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal
CC residue amino acid 810 to 906, or having a minimal amino acid sequence
CC (NS2/3) protease Also included are (1) a composition (C) comprising a sufficient concentration of lauryldiethylamine oxide (LDAO)
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CC comprising a sufficient concentration of lauryldiethylamine oxide (LDAO)
CC comprising a sufficient concentration of lauryldiethylamine oxide (LDAO)
CC comprising a sufficient concentration of lauryldiethylamine oxide (LDAO)
CC control agent, refolding the protease in the presence of a
CC reducing agent, and LDAO in the presence of reduced concentration of the
CC reducing agent or a polar additive, (4) producing (M1) an active NS2/3
CC protease, involving isolating the protease by contacting it with a
CC containing an activation detergent to induce auto-cleavage of the NS2/3
CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3
CC protease; (6) measuring (M3) the active NS2/3 protease and produce
CC cleavage products or their fragments, and measuring the presence or
CC absence of uncleaved NS2/3 protease, cleavage products or their fragments of the presence of, or
CC absence of the potential inhibitor of auto-cleavage activity of an
CC uneful for detailed biochemical characterisation of the emount of uncleaved
CC uneful for detailed biochemical characterisation of the protease in the development of in vitro assays for screening novel inhibitors of
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CC intertory for the protease of the NS2/3 protease of the NS2/3 protease. The protease o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV; enzyme; protease; NS2/3 (815-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 41; Page 59-60; 67pp; English
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RESULT 8
ABG32191
ID ABG3
XX ABG3
XX ABG3
XX ABG3
XX ACC
DE HCV
XX HCV;
KW CChro
KW CChro
KW CChro
XX Hepa
XX Hepa
XX WO20
XX Hepa
XX WO20
XX WO1;
XX WPI;
XX Nove
PT Useff
PT Leng
XX Nove
PT Leng
XX Nove
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XX Disc
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Best Local S
Matches 303
                                         Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                                                                                                                                                                                                                                                                                                    HCV; enzyme; protease; NS2/3 (904-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiniflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.
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Pred. No. 4e-146;
0; Mismatches 0
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Disclosure; Page 65-66; 67pp; English

CC Ineight HCV (hepatitis C virus) non-structural (NS)2/3 procease (referred CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence CC from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC NS2/3 protease. Also included are (1) a composition (C) comprising a sufficient concentration of lauryldiethylamine oxide (IDAO) CC comprising a sufficient concentration of lauryldiethylamine oxide (IDAO) CC comprising a sufficient concentration of lauryldiethylamine oxide (IDAO) CC comprising as sufficient concentration of lauryldiethylamine oxide (IDAO) CC comprising as sufficient concentration of lauryldiethylamine oxide (IDAO) CC comprising as sufficient concentration of lauryldiethylamine oxide (IDAO) CC concentration as ABG32198; (3) protease; (2) a NS2/3 inhibitory peptide concentration gagent, refolding the protease in the presence of a chatropic agent or a golar additive; (4) producing (M2) an active NS2/3 CC protease, involving isolating the protease by contacting it with a creducing agent or a golar additive; (4) producing (M2) an active NS2/3 protease; (5) measuring (M3) the auto-cleavage activity of NS2/3 CC protease; (6) measuring (M3) the auto-cleavage activity of NS2/3 protease; (7) measuring the active NS2/3 protease produced by M2 CC cleavage products or their fragments, and measuring the presence or cative NS2/3 protease, involving incubating the active NS2/3 protease produced by M2 CC absence of the potential inhibitor; of auto-cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of a cative NS2/3 protease, involving carrying out M3 in the presence of cative NS2/3 protease, involving carrying out M3 in the protease is consistent of the development of in vitro assays for screening novel inhibitors of an inhibitors of an inhibitors of inhibitors of active NS2/3 protease is useful for high level production of protease. The consistent of the consistent of the c devoid of autocatalytic activity

Ş 밁 Ś В Ś 뭕 밁 Ś 밁 Ş Ş 멂 Query Match Best Local S Matches 301 316 241 256 181 196 121 136 302; 16 61 76 Н Similarity LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW 135 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDEIPVESMET 315 GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH <u>LRDLAVAVEPVIFSDMEVKIITWGADTAAAGDIISGLPVSARRGREILLGPADNFEGQGW</u> AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALIGTYVVDHLTPLQDWAHAG 75 TMR 318 Conservative 89.2%; <u>,</u> Score 1580; DB 5; Pred. No. 2.1e-145; 0; Mismatches 1; Indels ٥. 120 195 240 180 60 0

Sequence 303

Length 303;

RESULT ABG3218 ABG32189; ABG32189 standard; protein; 303 AA

BXXXU

05-NOV-2002

(first entry)

HCV protease NS2/3 truncation 904-1206/His952Ala

HCV; enzyme; protease; NS2/3 (904-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.

Hepatitis C virus

Misc-difference Location/Qualifiers

/note= "Wild-type His substituted by

WO200248375-A2

20-JUN-2002

13-DEC-2001; 2001WO-CA001796

15-DEC-2000; 2000US-0256031P

(BOEH) BOEHRINGER INGELHEIM CANADA LTD.

Thibeault D, Ů, Maurice R, Pilote L,

Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.

Example 7; Fig 8; 67pp; English

CC length HCV (hepatitis C virus) non-structural (NS)2/3 procease (referred CC length HCV (hepatitis C virus) non-structural (NS)2/3 procease (referred CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence CC from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC (NS2/3) protease. Also included are (1) a composition (C) comprising a sufficient concentration of lauryldathylamine oxide (LDAO) CC comprising as ABG32198; (3) protease; (1) a refolded, inactive HCV NS2/3 protease, involving isolating the protease in the presence of a chaotropic agent, and LDAO in the presence of a protease, involving dislating refolded inactive NS2/3 inhibitory peptide CC chaotropic agent or a polar additive; (4) producing (M1) an active NS2/3 (C protease, involving diluting refolded inactive NS2/3 inhibitory peptide CC chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 protease; (5) measuring (M3) the auto-cleavage activity of NS2/3 protease; (6) measuring (M3) the auto-cleavage activity of NS2/3 protease; (6) measuring (M3) the auto-cleavage of the presence of and produce cleavage products or their fragments, and measuring the presence of and produce apsence of incleaved NS2/3 protease, cleavage products or their fragments, and measuring the presence of and protease, involving incubating the active NS2/3 protease produced by M2 (C protease, involving incubating the active NS2/3 protease and produce cleavage produces or their fragments or their fragm

89.2%; Score 1579; BB ហ •• Length 303

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RESULT 10
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The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV; enzyme; protease; NS2/3 (904-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.
                                                                                 Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                                                                                                                                                                        20-JUN-2002
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                                                         Example 7;
                                                                                                                                              WPI; 2002-599511/64.
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Conservative
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122. .123
/note= "Wild-type L
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RESULT 11
ABG32188
ID ABG32
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AC ABG32
XX
DT 05-NC
XX
DE HCV I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ce residue amino acid 810 to 906, or having a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC NSZ/3 protease. Also included are (1) a composition (C) comprising an isolated HCV NSZ/3 protease selected from full length NSZ/3 protease, or cits truncation or a mutated sequence, where the protease is in a solution comprising a sufficient concentration of lauryldiethylamine oxide (IDAO) to prevent auto-cleavage of the protease; (2) a NSZ/3 inhibitory peptide grotease, involving isolating the protease in the presence of a creducing agent, refolding the protease in the presence of a creducing agent, and IDAO in the presence of reduced concentration of the containing agent or a polar additive; (4) producing (M2) an active NSZ/3 protease, involving diluting refolded inactive NSZ/3 protease in a medium containing an activation detergent to induce auto-cleavage of the NSZ/3 compresses; (5) measuring (M3) the auto-cleavage activity of NSZ/3 compresses; (5) measuring (M3) the auto-cleavage activity of NSZ/3 compresses; involving incubating the active NSZ/3 protease and produce cleavage products or their fragments, and measuring the presence or containing a potennial inhibitor of auto-cleavage activity of an active NSZ/3 protease, involving carrying out M3 in the presence of contactive NSZ/3 protease, involving carrying out M3 in the presence of out absence of the potential inhibitor, comparing the amount of uncleaved NSZ/3 protease, cleavage products or their fragments. The protease is cuseful for detailed biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of notease is settled biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of contactive to their fragments. The protease. The contactive to the full length NSZ/3 protease. The material inhibitors of the carrying out of the carrying out of the carrying out of the carrying out of the carrying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 301; Conserv
                     HCV protease NS2/3 truncation mutant 915-1206.
                                                                05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 301
                                                                                                                                                        ABG32188 standard; protein; 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RL--PITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                                                                                                                                                                                                                                                                                TMR 318
                                                                                                                                                                                                                                                                                                                                                             RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.7%;
ilarity 99.3%;
Conservative
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                                                                  (first entry)
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Pred. No. 1.9e-144;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 301;
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IFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQ 146
                                                                      AQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPV 86
                                        YVYDHLTPLQDWAHAGLRDLAVAVEPV
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The invention relates to an isolated polypeptide consisting of a fullcalled as NS2/3 (810-1206)), or its truncation, having as its N-terminal
caresidue amino acid 810 to 906, or having a minimal amino acid sequence
care from residues 904 to 1206 of hepatitis C virus (HCV) lb-40 full-length
care (NS2/3) protease. Also included are (1) a composition (c) comprising a sufficient concentration of lawyldiethylamine oxide (LDAO)
care to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide
cappearing as ABG22198; (3) produces in the presence of a
cappearing as ABG22198; (3) produces by contacting it with a
cappearing agent, refolding the isolated protease by contacting it with a
cappearing agent or a polar additive; (4) producing (M1) an active NS2/3
caprotease, involving isolating refolded inactive your active NS2/3
caprotease; involving diluting refolded inactive your active NS2/3
caprotease; involving incubating the auto-cleavage of the NS2/3
caprotease; involving incubating the auto-cleavage of the NS2/3
caprotease; involving incubating the auto-cleavage of the NS2/3
caprotease; involving incubating the active NS2/3 protease and produce
cappearing an activation detergent to induce auto-cleavage of the NS2/3
caprotease; involving incubating the active NS2/3 protease and produce
cappeared (5) measuring (M3) the auto-cleavage products or their fragments
cappeared (6) screening a potential inhibitor of auto-cleavage activity of NS2/3
cappotease; involving incubating the active NS2/3 protease produced by M2
cappote of the potential inhibitor of auto-cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of an active NS2/3 protease, involving carrying out M3 in the presence of an active NS2/3 protease, cleavage products or their fragments. The protease is
cappeared of the potential inhibitor, comparing the amount of uncleaved
cappearing as a serious conducts or their fragments. The protease is
cappeared of the protease windown to the enzymes and in the presence of the Query Match Best Local S Matches 292 Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation. Hepatitis C virus. Synthetic. HCV; enzyme; protease; NS2/3 (915-1206); hepatitis C virus inforchronic liver disease; cirrhosis; end-stage liver disease; virus hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; Sequence 292 Thibeault D, (BOEH) BOEHRINGER INGELHEIM CANADA LTD. 15-DEC-2000; 2000US-0256031P 13-DEC-2001; 2001WO-CA001796 20-JUN-2002 WO200248375-A2 chaotropic agent; 292; Similarity 86.5%; Score 1532; Ilarity 100.0%; Pred. No. 9. Conservative 0; Mismatches AA; Lamarre mutant; mutein. ū NS2/3 (915-1206); hepatitis C virus infection; cirrhosis; end-stage liver disease; virucide; English. Maurice R, Score 1532; DB 5; I pred. No. 9.5e-141; 0; Mismatches 0; Pilote L, Length 292; Pause Indels Þ 0 Gaps

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The invention describes a self-replicating hepatitis C virus (HCV) coplynucleotide molecule comprising a 5'-non translated region (NTR), cc where guanine at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein; and a 3'-NTR region. The self-cc replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating potential inhibitors of HCV replication. The HCV RNA molecule is also cuseful for efficiently establishing cell culture replication. The self-cc replicating polynucleotide molecule contains a 5'-NTR, where G at constituent is substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the CG (2042) C/R mutations, transduces and/or replicates with greater cc efficiency. This amino acid sequence represents a mutant of the hepatitis complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note:
                                                                                                                                                                                                                                                                                                New self-replicating RNA molecules from Hepatitis C virus (HCV), which possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
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                                                                                                                                                                                                                                                                      Claim 3; Page; 140pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 882
                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOEH ) BOEHRINGER INGELHEIM CANADA LTD
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                                                                                                                                                                                                                                                                                                                                                                                                      Pause A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Met substituted by Thr"
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                                                                                                                                                                                                                                                                      English
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RESULT 13
ABG30591
ID ABG30
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Matches
New self-replicating RNA molecules from Hepatitis C virus (HCV), possess enhanced transduction or replication efficiency, useful ^{\rm 1}
                                                                                                                                                                                                                        Misc-difference
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                                                                                                           22-DEC-2000; 2000US-0257857P
                                                                                                                                                                                   WO200252015-A2.
                                                                                                                                                                                                                                                                                                                     Self-replicating; hepatitis C'virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                        ABG30591;
                                     WPI; 2002-575382/61.
                                                            Kukolj
                                                                                                                                  20-DEC-2001; 2001WO-CA001843
                                                                                                                                                           04-JUL-2002.
                                                                                                                                                                                                                                                                                            Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                21-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2201 AA;
                                                                                    (BOEH ) BOEHRINGER INGELHEIM CANADA LTD
                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
                                                           ر<u>،</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 94.7
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGSKTLAGPKGPITOMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLLAPITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
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                                                            Pause
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398
                                                                                                                                                                                                                     /note= "Wild type Ser substituted by
                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                         /label= Arg, Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.4%;
94.7%;
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Pred. No. 2.1e-139;
9; Mismatches 7;
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                                                                                                                                                                                                                                  Gly"
s (HCV), which useful for
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RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET 315

RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET

394

334

GAGSKTLAGPKGPITQMYINVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 255

RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH 195

RILAPITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYH

274

정 유

장 유

316

TMRT

319

136 215 196 196 275 256 335

395

TMRS

RESULT 14
ABG30600
ID ABG30
XX ABG30
XX ABG30
XX ABG30
XX 21-OC
XX Hepat
XX SelfXX cell
XX SelfXX SelfXX SelfXX Hepat
XX Hepat
XX

ABG30600; 21-OCT-2002

(first entry)

Key Misc-difference

Location/Qualifiers 882

Hepatitis C virus. Synthetic.

ABG30600 standard; protein;

2201

Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.

Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant

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                                                                                                                                                         Query Match
Best Local Similarity
Matches 288; Conserv
                                                                                                                                                                                                                                       Sequence 2201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page; 140pp; English.
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LRDLAVAVEPVVFSDMETKVITWGADTAACGDIILGLPVSARRGREIHLGPADSLEGQGW
                               LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW 135
                                                                                                                 AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
                                                                               AGITKVPYFVRAHGLIRACMLVRKVAGGHYVQMALMKLAALTGTYVYDHLTPLRDWAHAG
                                                                                                                                                             Conservative
                                                                                                                                                                              86.4%;
                                                                                                                                                             9
                                                                                                                                                           Score 1531; DB 5;
Pred. No. 2.1e-139;
9; Mismatches 7;
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                                                                                                                                                                                                                             RLLAPITAYSQQTRGLLGCIITSLTGRDXNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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TMRS 398
                                                      RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET 394
                                                                                                                                                                 GAGSKTLAGPKGPITOMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 255
                                                                                                                                                                                                     RLLAPITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
                                                                                                                                                                                                                                                                          <u>LRDLAVAVEPVVFSDMETKVITWGADTÄACGDIILGLPVSARRGREIHLGPADSLEGQGW</u>
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 1531; DB 5;
Pred. No. 2.1e-139;
9; Mismatches 7;
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RESULT 15
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ABG30581
ABG30581
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AX ABG30
AX Self-
KW Self-
KW Self-
KW Cell
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Best Local Similarity
Matches 288; Conserv
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                               GAGSKTLAGPKGP ITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                 RLLAPITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
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GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVR
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Search o Job time	Вb	γQ	DЪ	Qy
Search completed: May 6, 2004, 09:30:43 Job time : 46.463 secs	395 TMRS 398	316 TMRT 319	335 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET 394	256 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET 315

Run on:

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protein search, using sw

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

Minimum Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database Title: Perfect score: Total number of hits satisfying chosen parameters: Scoring table: Sequence: score greater Pred. No. DB seq length: 0 seq length: 2000000000 PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* BLOSUM62 Gapop 10.0 , 283366 seqs, 96191526 residues 1 MKKKKLEHHHHHTSAGITK... US-10-650-585-4 1771 6, 2004, 09:22:36 ; Search time 10.8777 Seconds (without alignments) 2953.573 Million cell updates/sec Gapext 0.5TTMRTSSAWRHPQFGGKKKK 334

is derived is the number of results predicted by chance to have a sater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

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genome polyprotein	hugl protein - hum	genome polyprotein	conserved hypothet		structural protein	aconitate hydratas	hypothetical prote	structural protein	CDA peptide synthe	hypothetical prote	transferrin precur	cobN protein homol	tetracycline 6-hyd	DNA-directed DNA p	conserved hypothet	polyprotein - marm	polyprotein - dour		genome polyprotein		genome polyprotein					genome polyprotein		genome polyprotein	scription	

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genome polyprotein - hepatitis C virus (strain J)
N;Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Accession: A39253; PS0086
R;Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimot Proc. Natl. Acad: Sci. U.S.A. 87, 9524-9528, 1990
A;Ritle: Molecular cloning of the human hepatitis C virus genome from Japanese patients
A;Reference number: A39253; MUID:91088550; PMID:2175903
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A;Title: Japanese isolates of the non-A, nor A;Reference number: P80085
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                                                                                            RLLAPITAYSQQTRGLLGCIITSLTGRDXXQVDGEVQVLSTATQSFLATCVNGVCWTVYH
                                                            GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                               LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW
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         RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                    RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
                                                                                                                                                    LRDLAVAVEPVVFSDMETKLITWGADTAACGDIISGLPVSARRGKEILLGPADSFGEQGW
                                                                                                                                                                                                          AGITRVPYFVRAQGLIRACMLVRKVAGGHYVQMAFMKLAALTGTYVYDHLTPLRDWAHAG
                                                                                                                                                                                                                                       AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
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                                                                                                                                                                                                                                                                                86.3%;
94.1%;
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                                                                                                                                                                                                                                                                   Score 1528; DB 1;
Pred. No. 7.1e-121;
2; Mismatches 6;
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                        RESULT 4
S18030
          genome polyprotein -
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C; Species: hepatitis C virus
C; Species: host Homo sapiens (man)
C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001
C; Accession: A40244
R; Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
Virology 188, 102-113, 1992
A; Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the !
A; Crosesion: A40244; MUID: 92230206; PMID: 1314449
A; Accession: A40244
A; Accession: A40244; MUID: 92230206; PMID: 1314449
A; Accession: A40244
A; Croses-references: GB: M84754
A; Croses-references: G
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                                                                                             RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                      GAGSKTLAGPKGPITQMYTNVDQDLVGWHAPQGARSLTPCTCGSSDLYLVTRHADVIPVR
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Pred. No. 9e-120;
3; Mismatches
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tein M; hepacivirin
nonstructural prote
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hepatitis

C virus

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A;Cross-references: EMBL:XS1591

A;Cross-references: EMBL:XS1591

A;Note: this sequence is inconsistent with the nucleotide translation A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for as Trp, and TTC for residue 771 as Ser

A;Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)

C;Superfamily: hepatitis C virus genome polyprotein C;Superfamily: hepatitis C virus predicted cEPM>
F;116-191/Product: envelope protein M; #status predicted cMEE>
F;130-1006/Product: nonstructural protein NS2 #status predicted cNS2>
F;130-1237/Region: nucleotide-binding motif B
F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted cN4A>
F;106,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carb
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A;Variety: isolate JK1
C;Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 23-Mar-2001
C;Accession: $18030; $33570; A48332; $18029
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X61596; NID:g59478; PIDN:CAA43793.1; PID:g59479
A;Experimental source: isolate JK1 from an individual
R;Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A;Title: Sequence analysis of putative structural regions of hepatitis C
A;Reference number: A48332; MUID:93119270; PMID:8380322
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A;Description: A whole genome of hepatitis C virus cDNA was isolated from a single
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A; Residues: 1-3010 < HON>
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A; Residues: 1-547, 'T', 549-62
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                                                                                                         RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
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92.1%;
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Pred. No. 2.1e-117;
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RESULT

A;Reference number:

Library,

Accession: S40770

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F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-189/Product: major envelope protein E #status predicted <MSE>
F;390-729/Product: monstructural protein NS1 #status predicted <NS1>
F;700-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: bexH motif
F;1316-1319/Region: bexH motif
F;1316-1319/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4a #status predicted <N4B>
F;1863-2013/Product: nonstructural protein NS5 #status predicted <N4B>
F;1863-2013/Product: nonstructural protein NS5 #status predicted <N4B>
F;1966,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,224
                                              genome polyprotein - hepatitis C virus N;Contains: capsid protein C; envelope protein NS4a; nonstructural protein NS4b; C;Species: hepatitis C virus C;Date: 19-May-2000 #sequence_revision 19-NC;Accession: S40770; PC1285
R;Okamoto, H. submitted to the EMBL
                                                                                                                                                                                                           RESULT
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A; Cross-references: EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g329771
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; capsid protein; enveloge protein; glycoprotein; hydrolase;
F; 2-115/P; coduct: capsid protein C #status predicted <CPC>
F; 2-115/P; coduct: capsid protein C #status predicted <CPC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type:
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//Contains: capsid protein C, envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
;Species: hepatitis C virus
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|Species: 1992 #sequence_revision 31-Mar-1992 #text_change 19-Jan-2001
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Pred. No. 1e-116;
2; Mismatches 1
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A; Molecule type: genomic RNA
A; Residues: 1-513 <0X2>
A; Cross-references: GB:D00831; NID:g221511; PIDN:BAA00705.1; PID:g221512
A; Cross-references: GB:D00831; NID:g221511; PIDN:BAA00705.1; PID:g221512
A; Experimental source: isolate HC-J1
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; P:g2-115/product: capsid protein C #status predicted <CPC>
F; 216-191/Product: envelope protein M #status predicted <MED>
F; 102-389/Product: major envelope protein E #status predicted <NS1>
F; 130-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F; 130-105/Product: hepacivirin #status predicted <NS3>
F; 1310-1317/Region: nucleotide-binding motif B
F; 1316-1319/Region: DEXH motif
F; 1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F; 1316-1319/Region: DEXH motif
F; 1616-1862/Product: nonstructural protein NS4a #status predicted <N4B>
F; 2014-3011/Product: nonstructural protein NS5 #status predicted <N4B>
F; 2014-3011/Product: nonstructural protein NS5 #status predicted <N4B>
A;Reference number: A39166; MUID:91172826; PMID:1848704
A;Accession: A39166
A;Molecule type: mRNA
A;Residues: 1-3011 <CHO>
A;Cross-references: GB.M62321; NID:g329873; PIDN:AAA45676.1;
R;Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer,
J. Gen. Virol. 73, 1131-1141, 1992
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GNWVC3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome polyprotein - hepatitis C virus (strain HCV-1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis
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Pred. No. 2.4e-110;
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                                                                                   PID:g329874
J.F.; Follett,
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A, Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to ex A, Reference number: PQ0393; MUID:92268871; PMID:1316939
A, Residues: pQ0403
A; Molecule type: genomic RNA
A, Residues: 1577-1633 < CCHA
A, Cross-references: DDBJ;D10128
A, Experimental source: isolates E-b16
A, Accession: PQ0404
A, Status: prelininary
A, Molecule type: genomic RNA
A, Residues: 1577-1633 < CCH2
A, Status: prelininary
A; Molecule type: genomic RNA
A, Residues: 1577-1633 < CCH2
A, Experimental source: isolates E-b17
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
F; 1-115/Product: major envelope protein M #status predicted <EPM>F; 192-389/Product: monstructural protein NS1 #status predicted <NS1>F; 1907-1615/Product: monstructural protein NS1 #status predicted <NS2>
F; 1007-1615/Product: hepacivirin #status predicted <NS3>F; 1007-1615/Product: nonstructural protein NS1 #status predicted <NS2>
F; 1316-1319/Region: nucleotide-binding motif A (P-loop)
F; 1312-1317/Region: nucleotide-binding motif B (P-loop)
F; 1316-1916/Product: nonstructural protein NS4a #status predicted <N4A>
F; 1863-2013/Product: nonstructural protein NS4a #status predicted <N4B>
F; 2014-3011/Product: nonstructural protein NS4a #status predicted <N4B>
F; 2014-3011/Product: nonstructural protein NS5 #status predicted <N4B>
F; 196, 209, 234, 305, 325, 417, 423, 430, 448, 476, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2077, 224
                                                                                   genome polyprotein - hepatitis C virus (strain H)
N;Contains: capsid protein C; envelope protein M; hepacivirin
protein NS4a; nonstructural protein NS4b; nonstructural prote
C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_chang
C;Accession: A36814; A41546
R;Inchauspe, G; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff,
submitted to GenBank, July 1992
A;Description: Genomic structure of the human prototype strain
                                                                                                                                                                                                                                                                                                                                  RESULT
GNWVCH
A;Accession: A36814
A;Molecule type: genomic
A;Residues: 1-3011 <INC>
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                                                                      A; Reference number: A36814
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Best Local Similarity
Matches 256; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TMRT 319
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Pred. No. 6.3e-110;
5; Mismatches 23;
                                                                                                                                                                                        #text_change 19-Jan-2001
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C;Species: hepatitis C virus
C;Atte: 19-May-2000 #sequence_revision 19-May-2000 #text_ch:
C;Atte: 19-May-2000 #sequence_revision 19-May-2000 #text_ch:
C;Accession: JC5620
R;Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P
Biochem. Biophys. Res. Commun. 236, 44-49, 1997
Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A;Title: The complete coding sequence of hepatitis C virus
A;Title: The complete coding sequence of hepatitis C virus
A;Reference number: JC5620; MUID:97366593; PMID:9223423
A;Reference number: JC5620, MUID:97366593; PMID:9223423
A;Accession: JC5620
A;Molecule type: mRNA
A;Residues: 1-3014 <CHA>
A;Residues: 1-3014 <CHA>
A;Residues: 1-3014 <CHA>
A;Residues: 1-3015 <CHA>
A;Cross-references: GB:Y13184
A;Experimental source: genotype 5a, which predominates in South A;Experimental source: genotype 5a, which predominates in South A;Experimental source: uncleotide sequence is not comp C;Superfamily: hepatitis C virus genome polyprotein C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; F;2-115/product: capsid protein C #status predicted <CPC>
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C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstructural
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
F;1115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <NES>
F;120-389/Product: nonstructural protein NS1 #status predicted <NS1>
F;300-729/Product: nonstructural protein NS2 #status predicted <NS2>
F;300-729/Product: hepacivirin #status predicted <NS2>
F;1307-1815/Product: hepacivirin #status predicted <NS2>
F;1307-1817/Product: hepacivirin #status predicted <NS2>
F;1312-1317/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1863-2013/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N85>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <N85>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <N85>
F;2014-3017/Product: nonstructural protein NS5 #status predicted <N85>
F;2014-3017/Product: nonstructural protein NS5 #status predicted <N85>
F;2014-3017/Product: nonstructural protein NS5 #status predicted <N85>
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JC5620
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
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Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A;Tille: Genomic structure of the human prototype strain
A;Reference number: A41546; MUID:92052256; PMID:1658800
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Best Local
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bedee, S.; Lee, D.H.; Sugitani, M.; Nasofi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.3%; Score 1386; DB 1
83.6%; Pred. No. 8e-109;
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                                                                                                     complete in this
                                                                                                                               South
                                                                                                                                                                                                                                                                                                             genotype 5a,
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f, M.; Prince,
                                      P-loop;
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F;1316-1321/Region: nucleotide-binding motif B
F;1320-1323/Region: DEXH motif
F;1320-1323/Region: DEXH motif
F;1360-1366/Product: nonstructural protein NS4a #status predicted <N4A>
F;1867-2017/Product: nonstructural protein NS4b #status predicted <N4B>
F;2018-3033/Product: nonstructural protein NS5 #status predicted <N05>
                                                                                                                                A;Cross-references: GB:000944; NID:g221650; PIDN:BAA00792.1; PID:g221651
A;Experimental source: isolate HC-J6 from a Japanese individual
C;Superfamily: hepatitis C virus genome polyprotein; serine processes ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine processes ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine processes ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine processes ATP; glycoprotein; protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <MEE>
F;192-389/Product: major envelope protein E #status predicted <MEE>
F;390-733/Product: nonstructural protein NS1 #status predicted <NS1>
F;734-1010/Product: hepacivirin #status predicted <NS2>
F;101-1619/Product: hepacivirin #status predicted <NS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome polyprotein - hepatitis C virus (isolate HC-J6)
N/COntains: capsid protein C, envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: genomic A; Residues: 1-3033 < OKA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H. J. Gen. Virol. 72, 2697-2704, 1991
A;Title: Nuclectide sequence of the genomic RNA of hepatitis A;Reference number: JQ1303; MUID:92044440; PMID:1658196
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F;1313-1318/Region: nucleotide-binding motif B
F;1317-1320/Region: DEXH motif
F;1617-1863/Product: nonstructural protein NS4a #status predicted <N4A>
F;1617-1861/Product: nonstructural protein NS4b #status predicted <N4B>
F;1864-2014/Product: nonstructural protein NS5 #status predicted <NS5>
F;2015-3014/Product: nonstructural protein NS5 #status predicted <NS5>
F;2210-2249/Region: interferon sensitivity determining #status predicte
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Pred. No. 5.3e-96;
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A;Molecule type: genomic RNA
A;Residues: 2678-2754 <CHA>
A;Cross-references: DDBJ:D10134
A;Cross-references: DDBJ:D10134
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A;Title: Distribution of plural HCV types in Japan.
A;Title: Distribution of plural HCV types in Japan.
A;Reference number: PQ0559
A;Molecule type: mRNA
A;Residues: 2678-2729 <KAT>
A;A;Cross-references: GB:D10562; GB:D90518; NID:9221523; PIDN:BAA01418.1; PID:9221524
A;Cross-references: GB:D10562; GB:D90518; NID:9221523; PIDN:BAA01418.1; PID:9221524
A;Cross-reference mmber: PQ0554; MUID:92068204; PMID:1720309
A;Molecule type: MID:92068204; PMID:1720309
A;Mol
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GNWVUB

genome polyprotein - hepatitis C virus (strain HC-J8)

genome polyprotein C; envelope protein M; hepacivirin (EC 3.4.21.98)

N; Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)

Protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C; Species: hepatitis C virus

C; Date: 31.Dec-1992 #sequence revision 31-Dec-1992 #text_change 19-Jan-2001

C; Accession: A40250; PQ0397; PQ0559

C; Accession: A40250; PQ0397; PQ0559

R; Okamoto, H.; Kurai, K.; Okada, S.I.; Yamamoto, K.; Lizuka, H.; Tanaka, T.;

Virology 188, 331-341, 1992

A; Title: Full-length sequence of a hepatitis C virus genome having poor homol

A; Reference number: A40250; MUID:92230232; PMID:1314459

A; Accession: A40250

A; Molecule type: genomic RNA

A; Residues: 1-3033 COKA>

A; Fire Capacic CB, NORGES, CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:D10988; GB:D01221; NID:g221608; PIDN:BAA01761.1; PID:g221609 R;Chan, S.W.; McCmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship (A,Reference number: PQ0393; MUID:92268871; PMID:1316939
A;Accession: PQ0397
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Pred. No. 9.8e-91;
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RIERRET, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C. J. Gen. Virol. 79, 41-45, 1998
A; Title: Genomic analysis of two GB virus A variants isolated from A.Reference number: Z16486; MUID:98120818; PMID:9460920
A;Accession: T08841
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3005 <ERK>
A;Cross-references: EMBL:AF023425; NID:92828599; PIDN:AAC40502.1; C;Superfamily: hepatitis C virus genome polyprotein
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F;1320-1323/Region: DEXH motif
F;1620-1866/Product: nonstructural protein NS4a #status predicted <N4A>
F;1650-11866/Product: nonstructural protein NS4b #status predicted <N4B>
F;1867-2017/Product: nonstructural protein NS5 #status predicted <NS5>
F;2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,233,299,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,235
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Matches 97
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                                                                                                                                                                       VEGLPVVARRGDEVLVGVFPSVRALPPGFVPTAPVVV-MORGLGFFSVVKTSMLGRDERE
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                                         PGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSG
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                                                                                                                                                                                                                                                                                                                                                      Score 398.5; DB 2;
Pred. No. 5.3e-25;
5; Mismatches 125;
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         1123
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                                                   286
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Conserved hypothetical protein CC1155 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: G87392 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
G87392
                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <STO>
A;Cross-references: GB:AB005673; NID:g13422473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.; Mushahwar, I.K. J. Gen. Virol. 79, 41-45, 1998
A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys. A;Reference number: Z16486; MUID:98120818; PMID:9460920
A;Accession: T08839
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T08839
R;Erker, J.C.; Desai, S.M
J. Gen. Virol. 79, 41-45,
                                                                                                                                                                                                                                                A;Reference number: A87249;
A;Accession: G87392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: genomic RNA
A; Residues: 1-2970 < ERK>
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C;Species: 1
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Query Match 6.1%; Score 108; DB 2; Best Local Similarity 21.9%; Pred. No. 0.16; Matches 77; Conservative 36; Mismatches 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   olyprotein - marmoset hepatitis GB virus ; Species: marmoset hepatitis GB virus A; Date: 23-Jul-1999 #sequence_revision 23-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                   CC1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   891 YAHAGQVTRRTAEQLRQWGFALEPVAVHPEDCAMVRDAARTLSCGQSVHGKPVVARRGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 WAHAG-----LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMRTSSAW 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGSSDLYLVTRHADVIPVRRRGDSRGSLLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTTRSMGTCVNGVMYTTYHGSNARTLAAQMGPVNSRWWSASDDVAVYPLPVGAKCLEPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLIGVLNGV----WELPPGFVPTAPVVVH-HHGKGFFGVVKTSMTGWDETEHVGNVVVLG
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Pred. No. 2.7e-20;
P4; Mismatches 94; Indels 5
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23-Jul-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GALCHGTLGRTVELDLPAELCDFRGSSGSPILCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SRVTGIRYTKPW 1139
                                                                                                                                          PIDN:AAK23139.1; GSPDB:GN00148
  122;
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                                            Length 353;
Indels 116;
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Gaps
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A;Experimental source: FW3A cells
A;Note: sequence extracted from NCBI backbone (NCBIN:129148, NCBIP:129149)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Biol. Chem. 268, 8111-8122, 1993
A;Title: Molecular cloning of the cDNAs for the four subunits A;Reference number: A46642; MUID:93216788; PMID:8463324
A;Accession: B46642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
B46642
DNA-directed DNA polymerase (EC 2.7.7.7) alpha/DNA primase (EC 2.7.7.-) complex C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: B46642
C;Accession: B46642
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA;
A;Residues: 1-600 <MIY>
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Best Local S
Matches 55
   179
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                                                                                                                                                                                                                                                                                                                 Similarity
                                   ATCVNGVCWTVFHGAGSKTL--AGPKGPITQMYTNVDQDLVG
                                                                                                         LLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFL 182
                                                                                                                                            HAGTRDI-VSIQELIEAEEEEETLLSSYTTPSKGPLKRVSSTPETPLTKRSVAARSPRQ-
                                                                                                                                                                                  HAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDI--ISGLP-----
                                                                                                                                                                                                                       LAELCVLYRQTEDGMVSELIAFCTSAGKTCLTVDILNSFEYEVLNKKLSKAWHSASKDSG
                                                                                                                                                                                                                                                            LIRACMLVRKAAGGHYVQM-AFMKLAALT-----GTYVYDHL-----TPLQDWA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TP-LQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFRSGQGAVLLTGGLAAGLMFLVANGMLTALGESGALTPFLAVWAAPAIFG 341
                                                                        LLSPSS-----FSPSATPSQK-----YTSRTNR-----GEVVTTFGSAQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IFR----AAVCTRGVAKAVDFIPVESMETTMRTSSA-----
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                                                                                                                                                                                                                                                                                                 Conservative
 GLSWSGRGGSGSVSLKVVGDPEPLTGSYKAMFQQLMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                               24.8%;
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                                                                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                                                                                             Score 101; DB Pred. No. 1.3; 4; Mismatches
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                                                                                                                                                                                                                                                                                           71;
                                                                                                                                                                                                                                                                                                                                Length 600;
                                                                                                                                                                                                                                                                                             Indels
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215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.; Ui, M.; Hanaoka,
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                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                   -VSARRGREI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse DNA polymerase
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                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                              144
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Search completed: May 6, 2004, 09:37:14 Job time : 12.8777 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1 MKKKKLEHHHHHHTSAGITK......TTMRTSSAWRHPQFGGKKKK 334
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DAC_ACTSP
DAC_SCHPO
RPOC_PSEAE
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VST2_HEVRH
VST2_HEVMY
NRAM_IAWIL
UCP2_MOUSE
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POLG_HCVJ8
DPO2_MOUSE
TRFE_HORSE
VST2_HEVBU
VST2_HEVPA
PTPV_MOUSE
VST2_HEVME
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P27958 h genome po
P26660 h genome po
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P27425 equus cabal
P27425 equus cabal
P29326 hepatitis e
P70289 mus musculu
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P27436 t genome po
P07720 t genome po
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P075803 influenza a
Q8keq0 chlorobium
P03477 influenza a
O8bga77 auttus norv
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                       0 hepatitis
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                                                     EMBL; D11168; BAA01943.1; -. PIR; A45573; A45573. MEROPS; S29.001; -. MEROPS; U39.001; -.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_capsid.
                                                                                                                                  or send an email to license@isb-sib.ch).
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45	44	43	42	41	40	39	38	37	36	ა 5	34
81	18	81	81	81	81.5	81.5	81.5	82	82	82	82
4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6
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methanosarc	herpes simp	influenza a	arabidopsis	pseudomonas	gallus gall	rhodobacter	agrobacteri	homo sapien	spergillus	chlamydomon	chlamydia m

ALIGNMENTS

POLG	POLG_HCVJT	
	POLG_HCVJT STANDARD; PRT; 3010 AA.	
AC	(# - 1 - 2)	
	1993 (Rel. 25, Created)	
H H	UL-AFK-1993 (Rel. 25, Last annotation undate)	
DE	Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);	
DE	Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2	
DE	(GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)	
DE	(EC 3.4.22); Protease/helicase NS3 (P70) (Hepacivirin)	
DE	(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein	
H	NS48 (P27); Nonstructural protein NS5A (P56); Nonstructural protein	
E	NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].	
S	Hepatitis C virus (isolate HC-JT) (HCV).	
გ	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;	
გ		
×	NCBI_TaxID=31642;	
R		
4 5	MEDITANE PROPERTY.	
RA !	Tanaka T., Kato N., Nakagawa M., Ootsuvama Y., Cho M.J.,	
ŖΑ	Nakazawa T., Hijikata M., Ishimura Y., Shimotohno K.;	
RT	"Molecular cloning of hepatitis C virus genome from a single Japanese	
I XI	carrier: sequence variation within the same individual and among	
7 7	intected individuals.";	
3 8	- !	
88	-:- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are	
6	į	
റ്റ	-!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral	
38		
3 6	position,	
2 2	-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N)	
င္ပ	-!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a	
S	lipoprotein envelope. The envelope consists of two proteins:	
32	protein M and glycoprotein E. The nucleocapsid is a complex of	
36	DIFOCENT C AND MENA.	
ខ្លួ	CHIEFFIELD SACHESSE BELLAND IN SECTION SANIEL SAN.	
	entry is copyright. It is produced through a	
	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
	European Bioinformatics Institute. Ther	
	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Hearth but and for commercial	
	a license agreement (See h	

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c; IPR002519; HCV_env.
ro; IPR002511; HCV_NS1.
ro; IPR002511; HCV_NS1.
ro; IPR002511; HCV_NS1.
pro; IPR002518; HCV_NS4.
Pro; IPR002518; HCV_NS4a.
Pro; IPR001490; HCV_NS4a.
Pro; IPR001490; HCV_NS4a.
Pro; IPR001490; Hellcase_C2.
cerpro; IPR004109; Peptidase_C2.
cerpro; IPR004109; RNA_pol_DS_PS.
terpro; IPR007094; RNA_pol_DS_PS.
tempro; IPR007094; RNA_pol_DS_PS.
tempro; IPR007094; RNA_pol_PSVir.
fam; PF01543; HCV_capsid; 1.
fam; PF01543; HCV_NS1; 1.
Pfam; PF01553; HCV_NS1; 1.
Pfam; PF01560; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF010099; Viral_RdRP; 1.
Pfam; PF00999; Viral_RdP; 1.
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CELLULAR AMINOPERTIDASE.
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MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
                                                              Score 1533; DB 1;
Pred. No. 9.9e-124;
7; Mismatches 8;
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ATP-binding;
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01-AUG-1992 (Rel. 2
28-FEB-2003 (Rel. 2
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein P2);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS4B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate Japanese) (HCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDIJUS=91088550; PubMed=2175903;
MEDIJUS=91088550; PubMed=2175903;
Kato N., Hijikata M., Ootsuyama Y., Nakagawa M., Ohkoshi S.,
Sugimura T., Shimotohno K.;
Sugimura T., Shimotohno K.;
"Molecular cloning of the human hepatitis C virus genome from
"Molecular cloning of the human hepatitis.";
                                                                                                                                                                                            Kato N., Hijikata M., Nakagawa M., Ootsuyama Y., Muraiso K., Ohkoshi S., Shimotohno K.;
"Molecular structure of the Japanese hepatitis C viral genome.";
PEBS Lett. 280:325-328(1991).

1- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function and NS5 may play a role in the viral RNA replication.

1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                     {RNA}(N).

-! SUBUNIT: The virion of this virus is a nucleocapsid covered lipoprotein envelope. The envelope consists of two proteins protein M and glycoprotein E. The nucleocapsid is a complex protein C and mRNA.

-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLG
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                      DISCUSSION OF SEQUENCE PUBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Japanese patients with non-A, non-B hepatitis.";
Proc. Natl. Acad. Sci. U.S.A. 87:9524-9528(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           depacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CBI_TaxID=11116;
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Hijikata M., Nakagawa M., Ootsuyama Y., Muraiso
S., Shimotohno K.;
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InterPro; IPR00903; Cys Ser trypsin.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_core.
InterPro; IPR002513; HCV_NS1.
InterPro; IPR002513; HCV_NS4a.
InterPro; IPR002745; HCV_NS4a.
InterPro; IPR000745; HCV_NS4b.
InterPro; IPR000745; HCV_NS4b.
InterPro; IPR001650; HCV_NS4b.
InterPro; IPR001650; HCV_RdRP.
InterPro; IPR001160; HCV_RdRP.
InterPro; IPR001160; HCV_RdRP.
InterPro; IPR001160; Peptidase C29.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007096; RNA_pol_DS_PS.
InterPro; IPR007096; NNA_pol_PSvir.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01543; HCV_core; 1.
Pfam; PF01560; HCV_NS2; 1.
Pfam; PF01560; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF002907; Viral_RdRP; 1.
Pr0DDom; PD186062; HCV_NS1; 1.
Pr0DDom; PD186062; HCV_NS1; 1.
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Transmembrane; (
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MEROPS; U39.001;
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PIR; A39253; GNWVCJ.
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 Glycoprotein; 1; Coat protein;
                                                                                                                                                                                                                                                                                           Nonstructural
CELLULAR AMINOPEPTIDASE.

CAPSID PROTEIN C (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
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Matches 286
                      **SEQUENCE FROM N.A.

**MEDLINE-92230206; PubMed=1314449;

**MEDLINE-92230206; PubMed=1314449;

**A Chen P.J., Lin M.H., Tai K.F., Liu P.C., Lin C.J., Chen D.S.;

**A Chen P.J., Lin M.H., Tai K.F., Liu P.C., Lin C.J., Chen D.S.;

**A Chen P.J., Lin M.H., Tai K.F., Liu P.C., Lin C.J., Chen D.S.;

**A Chen P.J., Lin M.H., Tai K.F., Liu P.C., Lin C.J., Chen D.S.;

**A Chen P.J., Lin M.H., Tai K.F., Liu P.C., Lin C.J., Chen D.S.;

**The Taiwanese hepatitis C virus genome: sequence determination

**The Taiwanese hepatitis C virus genomic and antigenomic RNA.";

**Lin Virology 188:102-113 (1992)

**C Lin FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function of the viral RNA replication.

**C Lin CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the processition, Cys or Thr in P1 and Ser or Ala in P1'.

**C LIN ALL C. C. LIN ALL COMMONIA WITH ASP OR GLU in the P6 possition, Cys or Thr in P1 and Ser or Ala in P1'.

**C LIN ALL C. C. LIN ALL C. L
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SEQUENCE
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NCBI_TaxID=31645;
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Pred. No. 2.7e-123;
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pfam; pro1342; HCV_core; 1.
pfam; pro1539; HCV_core; 1.
pfam; pro1539; HCV_NS1; 1.
pfam; pro1539; HCV_NS2; 1.
pfam; pro1539; HCV_NS3; 1.
pfam; pro1539; HCV_NS3; 1.
pfam; pro1006; HCV_NS4a; 1.
pfam; pro1006; HCV_NS4b; 1.
pfam; pro1006; HCV_NS4b; 1.
pfam; pro10071; hclicase C; 1.
pfam; pro0098; Viral RdRp; 1.
proDom; pp186062; HCV_NS1; 1.
proDom; po186062; HCV_NS1; 1.
prolyprotein; Glycoprotein; Tran
polyprotein; Glycoprotein; Tran
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PIR; A40244; GNWVTW.
PDB; 1N64; 25-FEB-03.
PDB; 1N83; 08-APR-98.
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rPro; IPR001410;
rPro; IPR002522;
rPro; IPR002521;
rPro; IPR002531;
rPro; IPR002531;
rPro; IPR002531;
rPro; IPR001490;
rPro; IPR001490;
rPro; IPR001660;
rPro; IPR001600;
rPro; IPR001600;
rPro; IPR007094;
rPro; IPR007094;
rPro; IPR007094;
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   Glycoprotein; Transferase; RNA-directed RNA polymerase; Coat protein; Envelope protein; Helicase; ATP-binding; e; Nonstructural protein; Hydrolase; Serine protease;
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HCV core.

HCV NS1.

HCV NS2.

HCV NS4a.

HCV NS4b.

HCV NS4b.

HCV NS4b.

HCV NS6b.

HCV NS6c.

   Cys_Ser_trypsin.
DEAD.
                                                                                                                                                                                       REMOVED FROM CAPSID PROTEIN C BY THE CELLULAR AMINOPEPILIDASE.

CORE BROTEIN (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NSJ (POTENTIAL).

NONSTRUCTURAL PROTEIN NSZ (POTENTIAL).

PROTEASE/HELICASE NSJ (POTENTIAL).

NONSTRUCTURAL PROTEIN NSA (POTENTIAL).

POTENTIAL.

CHARGE RELAY SYSTEM (BY SIMILARITY).

ATP (POTENTIAL).
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	IG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBK POLG_HCVBC POLG_HCVBC Ol_AUG-1992 (Rel. 23, Created) Ol_AUG-1992 (Rel. 23, Last sequence update) (EC 3.4.21.98); Nonstructural protein NSA (Ps); Nonstructural protein NSA (Ps)	316 TMRT 3 : 1204 TMRS 1	256 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET 3	196 GAGSKTLAGÞKGPITQMYTNVDQDLVGWQAÞÞGARSMTÞCTCGSSDLYLVTRHAÐVIÞVR 25 	136 RLIAPITAYSQOTRGLIGCIITSLIGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH 19 	76 LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLÞVSARRGREILLGÞADNFEGOGW 13 	16 AGITKVPYFYRAQGLIRACMLVRKAAGGHYVQMAFMKLAALIGTYVVDHLIBLQDWAHAG 75 : ::	<pre>Match 85.5%; Score 1515; DB 1; Length 3010; DCal Similarity 92.8%; Pred. No. 3.5e-122; S 282; Conservative 13; Mismatches 9; Indels 0; Gaps</pre>	CARBOHYD 532 532 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 540 540 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 556 556 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 576 576 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 623 623 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 2041 2041 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 2077 2077 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 2074 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 2240 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 2529 N-LINKED (GLCNAC) (POTENTIAL) CARBOHYD 2788 2788 N-LINKED (GLCNAC) (POTENTIAL)

phosphorylation Eur. J. Biochem.

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WAYAN Y. LIY. Munshi S., Sardana V., Cole J.L., Sardana M., Yan Y., Li Y., Munshi S., Sardana V., Cole J.L., Sardana M., Steinkuehler C., Tomei L., de Francesco R., Kuo L.C., Chen Z.; IT "Complex of NS3 procease and NS4A peptide of BK strain hepatitis C virus: a 2.2-A resolution structure in a hexagonal crystal form.";

Protein Sci. 7:837-847(1998).

1. Protein Sci. 7:837-847(1998).

2. Protein Sci. 7:837-847(1998).

3. Protein Sci. 7:837-847(1998).

3. Protein Sci. 7:837-847(1998).

4. Protein Sci. 7:837-847(1998).

5. Protein Colliviry: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

5. Protein Colliviry: N nucleoside triphosphate = N diphosphate + (RNA)(N).

6. PRAN(N).

6. PRAN(N).

7. PROTEIN Mand glycoprotein E. The nucleocapsid covered by a lipoprotein cand mRNA.

7. PROTEIN SERIOUS TO PEPTIDASE FAMILY S29.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_sore.
InterPro; IPR002521; HCV_NS2.
InterPro; IPR002518; HCV_NS3.
InterPro; IPR002518; HCV_NS4a.
InterPro; IPR000745; HCV_NS4a.
InterPro; IPR000745; HCV_NS4a.
InterPro; IPR0002868; HCV_NS5a.
InterPro; IPR002166; HCV_NS5a.
InterPro; IPR007166; HCV_NS6a.
InterPro; IPR007109; RNA_pol_DS_PS.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PS_Vir.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01543; HCV_sore; 1.
Pfam; PF01543; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF01538; HCV_NS3; 1.
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Love R.A., Parge H.E., Wickersham J.A., Hostomsky Z., Habuka N.,
Moomaw E.W., Adachi T., Hostomska Z.;
"The crystal structure of hepatitis C virus NS3 proteinase reveals
trypsin-like fold and a structural zinc binding site.";
Cell 87:331-342(1996).
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MEDLINE-98227846; PubMed-9568891;
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. 237:611-618(1996).
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             Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00998; Viral_RdRP; 1.
ProDom; P0186062; HCV_NS1; 1.
SMART; SMO0487; DEXDO; 1.
SMART; SMO0487; DEXDO; 1.
Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Core protein; Coat protein; Envelope protein; Helicase; Serine protease; Transferase; Nonstructural protein; Hydrolase; Serine protease;
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NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
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(POTENTIAL)
(POTENTIAL)
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EMBL; PIR; ;

M58335;

A38465; GNWVTC.
1A10; 25 MAR-98.
1UXP; 114 JAN-98.
1NS3; 08 APR-98.
1C2P; 15 NOV-00.
1CSJ; 08 NOV-99.
1GX5; 09 APR-02.
1GX5; 07 APR-02.
1UV; 26 JUN-09.
80HM; 20 APR-99.

The nucleocapsid is a complex

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RESULT 5
POLG_HCV1
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Best Local S
Matches 279
                               ARDLINE-9177826; PubMed=1848704;

X MEDLINE-9177826; PubMed=1848704;

XA Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,

Ra Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,

Ra Bradley D.W., Xuo G., Houghton M.;

Renetic organization and diversity of the hepatitis C virus.";

Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455 (1991).

L Proc. Natl. Acad. Sci. U.S.A. 88:2451-255 (1991).

C -i- FUNCTION: The small proteins NS2B, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3

and NS5 may play a role in the viral RNA replication.

-i- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6

position, Cys or Thr in P1 and Ser or Ala in P1'.

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                          O1-AUG-1992 (Rel. 23, Created)
O1-AUG-1992 (Rel. 23, Last sequence update)
O1-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein P7, Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate 1) (HCV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
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HELIX
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SEQUENCE
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\{{\rm RNA}\}\,(N) . SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins:
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Pred. No. 4.5e-119;
2; Mismatches 13;
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MEROPS; U39.001; -.

InterPro; IPR001410; DEAD.

InterPro; IPR00252; HCV_capsid.

InterPro; IPR00252; HCV_core.

InterPro; IPR00251; HCV_NS1.

InterPro; IPR00251; HCV_NS2.

InterPro; IPR00251; HCV_NS4a.

InterPro; IPR000745; HCV_NS5a.

InterPro; IPR000745; HCV_RS4b.

InterPro; IPR001409; HCV_RS5a.

InterPro; IPR00160; HCV_RS6a.

InterPro; IPR00160; HCV_RS6b.

InterPro; IPR0017095; RNA_Dol_DS_PS.

InterPro; IPR007095; RNA_Dol_DS_PS.

InterPro; IPR007095; RNA_Dol_DS_PS.

InterPro; IPR007094; NNA_Dol_DS_PS.

InterPro; IPR007095; NNA_Dol_DS_PS.

InterPro; IPR007094; NNA_Dol_DS_PS.

InterPro; IPR007095; NNA_Dol_DS_PS.

InterPro; IPR007095; NNA_Dol_DS_PS.

InterPro; IPR007094; NNA_Dol_DS_PS.

INTERPRO; INTERPRO*

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Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
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MEROPS; U39.001;
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1A1V; 16-FEB-99.
1HEI; 25-NOV-98.
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                      POTENTIAL.

CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
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ATP (POTENTIAL)
DECH BOX.
N-LINKED (GLCNAC.
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MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).
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NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL)
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САЯВОНУЛ САЯВОНУЛ

Matches Query Match

16

Local

Similarity

79.0%;

Conservative

SEQUENCE

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OT 01-AUG-1992 (Rel. 23, Created)
OT 01-AUG-1992 (Rel. 23, Last sequence update)
OT 01-AUG-1992 (Rel. 23, Last sequence update)
OT 10-OCT-2003 (Rel. 42, Last annotation update)
OT 10-OCT-2003 (Rel. 42, Last annotation update)
OE Envelope glycoprotein [Contains: Capsid protein C (Core protein) (P22);
OE Envelope glycoprotein E1 (GP32) (GP35), Envelope glycoprotein E2
OE (GP66) (GP70) (NS1); Protein P7, Nonstructural protein NS2 (P21)
OE (EC 3.4.99.-); Protease/Helicase NS3 (P70) (Repacivirin)
OE (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
OE NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
OE NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
OC Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC NCBI TaxID=11108;
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                                                                                                                                                               PubMed=1658800;
edee S., Lee D.H.H.,
                                                                 the human prototype strain H of h American and Japanese isolates. U.S.A. 88:10292-10296(1991).
                       ANGSTROMS)
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Pred. No. 3.6e
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                       ITRANSPAC; TO4155; -.

INTERPRO; IPR009003; Cys_Ser_trypsin.

InterPro; IPR002522; HCV_capsid.

InterPro; IPR002521; HCV_core.

InterPro; IPR002521; HCV_NS1.

InterPro; IPR002519; HCV_NS2.

InterPro; IPR002518; HCV_NS3.

InterPro; IPR002518; HCV_NS4.

InterPro; IPR002518; HCV_NS5a.

InterPro; IPR002518; HCV_NS5a.

InterPro; IPR002166; HCV_NS5a.

InterPro; IPR002166; HCV_NS5a.

InterPro; IPR002166; HCV_RS5a.

InterPro; IPR002166; HCV_RS5a.

InterPro; IPR002166; HCV_RS5a.

InterPro; IPR007169; Peptidase_C29.

InterPro; IPR007199; RNA_pol_DS_PS.

InterPro; IPR007094; INC_Capsid; 1.

Pfam; PF01543; HCV_Core; 1.

Pfam; PF01543; HCV_NS1; 1.

Pfam; PF01538; HCV_NS3; 1.

R Pfam; PF01538; HCV_NS3; 1.

R Pfam; PF01506; HCV_NS4a; 1.

R Pfam; PF01006; HCV_NS4a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1HEI; 25-NOV-98.
PDB; 1AlV; 16-FEB-99.
PDB; 1AlR; 17-UUN-98.
MEROPS; S29.001; -.
MEROPS; U39.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I-FUNCTION: PROTEASE NS2 IS RESPONSIBLE FOR THE CLEAVAGE OF NS:
-I-FUNCTION: PROTEASE NS3 IS RESPONSIBLE FOR THE CLEAVAGE OF NS3-NS4A, NS4A-NS4B, NS4BS-NS5A AND NS5A-NS5B.
-I-FUNCTION: NS4A FORMS A COMPLEX WITH NS3 AND IS ESSENTIAL FOR ACTIVATION OF NS3.
-I-FUNCTION: NS5A SEEMS TO HAVE A TRANSCRIPTIONAL ACTIVATORY RO!
-I-FUNCTION: NS5B IS A RNA-DEPENDENT RNA POLYMERASE THAT PLAYS:
-I-FUNCTION: NS5B IS A RNA-DEPENDENT RNA POLYMERASE THAT PLAYS:
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MEDLLNE=98154321; PubMed=9493270;

Kim J.L., Morgenstern K.A., Griffith J.P., Dwyer M.D., Th

Murcko M.A., Lin C., Caron P.R.;

"Hepatitis C virus NS3 RNA helicase domain with a bound
oligonucleotide: the crystal structure provides insights
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YAO N., Hesson T., Cable M., Hong Z., Kwong A.D.,
"Structure of the hepatitis C virus RNA helicase of the Kapatina C virus RNA helicase of the Kapatina C virus RNA helicase of the Struct. Biol. 4:463-467 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCASSID COVERED B LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS; AND 22. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA. PTM: THE STRUCTURAL PROTEINS C, E1 AND 82 ARE PRODUCED BY PROTEOLYTIC PROCESSING BY THE HOST SIGNAL PEPTIDASES. SIMILARITY: THE NS2 PROTEASE BELONGS TO PEPTIDASE FAMILY U39. SIMILARITY: THE NS3 PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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Prince A.M.;
"Genomic structure of to virus: comparison with Natl. Acad. Sci.

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CRYSTALLOGRAPHY

(2.1)

SEQUENCE FROM N.A. MEDLINE=92052256; Inchauspe G., Zebe

Zebedee

3D-structure..
INIT_MET

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pfam; PF01506; HCV_NS5a; 1.
pfam; PF00271; helicase C; 1.
pfam; PF00999; Viral RARP; 1.
proDom; PD186062; HCV_NS1; 1.
smART; SM00487; DEXDC; 1.
protein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Polyprotein; Coat protein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
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CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C.
ENVELOPE GLYCOPROTEIN E1.
ENVELOPE GLYCOPROTEIN E2.
PROTEIN P7.
NONSTRUCTURAL PROTEIN NS2.
PROTEASE/HELICASE NS3.
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4A.
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POLG HCVJ6 STANDARD; PRT; 3033 AA.

ID POLG HCVJ6 STANDARD; PRT; 3033 AA.

POLG HCVJ6 STANDARD; PRT; 3033 AA.

P26670;
D1 AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 24), Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyproteein [Contains: Capsid protein C (Core protein) (P22);
DE Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
DE Envelope glycoprotein E2 (GP36); (GP36) (NOSTUCTURAL PROTEIN NS2 (P21))
DE (GC 3.4.21.9); Nonstructural protein NS4A (P4); Nonstructural protein
DE (EC 3.4.21.98); Nonstructural protein NS5A (P56); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
OS Hepatitis C virus (isolate HC-J6) (HCV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Pred. No. 4.8e-111;
7; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772CBB29CCD94753 CRC64;
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Hepacivirus. NCBI_TaxID=11113;

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A CRAMICHO H., Okada S.-I., Sugiyama Y., Kurai K., Lizuka H.,

Namachida A., Miyakawa Y., Mayumi M.;

"Nuclectide sequence of the genomic RNA of hepatitis C virus isolated

From a human carrier: comparison with reported isolates for conserved

RT and divergent regions.";

J. Gen. Virol. 72:2697-2704 (1991).

J. Gen. Virol. 72:2697-2704 (1991)
                                                                                                                                                                Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01560; HCV_NS2; 1.
Pfam; PF01006; HCV_NS4; 1.
Pfam; PF01001; HCV_NS4; 1.
Pfam; PF01001; HCV_NS4; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF00279; helicase C; 1.
Pfam; PF00998; Viral_RdRP; 1.
Pr0Dom; PF00998; Viral_RdRP; 1.
Pr0Dom; PF00998; Viral_RdRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002531;
InterPro; IPR002518;
InterPro; IPR00745;
InterPro; IPR001490;
InterPro; IPR002868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
work the by non-profit institutions as Its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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MEROPS; U39.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D00944; BAA00792.1; -. PIR; JQ1303; JQ1303. HSSP; P27958; 1HEI.
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                                                                  Transmembrane;
INIT_MET 1
                                                                                                            SMART; SM00487; DEXDC; 1.
Polyprotein; Glycoprotein;
Core protein; Coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007094; RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92044440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002522;
InterPro; IPR002521;
InterPro; IPR002519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR009003;
InterPro; IPR001410;
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                                                                                         Nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1658196;
                                                                                                              protein;
  115
191
                                                                                                                                                                                                                                                                                                                                                                                                                      HCV RdRP.
Helicase C.
Peptidase C29.
RNA pol DS PS.
RNA pol PSvir.
capsid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCV_capsid.
HCV_core.
HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS4a.
HCV_NS4a.
HCV_NS4b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cys Ser
                                                                                                       Transferase; RNA-directed RNA polymerase; Privelope protein; Helicase; ATP-binding;
Envelope protein; Helicase; ATP-bindii protein; Hydrolase; Serine protease. REMOVED FROM CAPSID PROTEIN C BY THE CELLULAR AMINOPEPTIDASE. CAPSID PROTEIN C (POTENTIAL). MATRIX PROTEIN (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions on
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RESUL POLG_ ID AC DI DI DI DE DE DE	B Q B Q B Q B Q B Q B Q B Q B Q B Q B Q	3 13 13
HCVU8 POLG HCV P26661; 01-AUG-1 01-AUG-1 28-FEB-2 Genome p Envelope (GP68) ((EC 3.4.	CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN CHAIN TRANSMEM ACT_SITE ACT_SITE ACT_SITE ACT_SITE ACT_SITE CARBOHYD	CHAIN
S (Rel 2 (Rel 2 (Rel 3 (Rel 3 (Rel 70) (NR) 70) (NR)	1011 1867 2018 347 347 1111 1111 1112 1136 1136 1132 1132 1132	
DARD; , Crea , Last , Last , Last , Last , Contai , Drote , Prote	1619 1619 1619 1619 1619 1619 1619 1619	383 733 1010
PRT; 3033 AA. sequence update) cannotation update) ns: Capsid protein C (Core protein) (P22); GP32) (GP35); Envelope glycoprotein E2 in P7; Nonstructural protein NS2 (P21) clicase NS3 (P70) (Hepacivirin)	PROTESSE HELICASE NSS POTENTIAL). NONSTRUCTURAL PROTEIN NSAA (POTENTIAL). RNA-DIRECTED RNA POLYMERASE (POTENTIAL). POTENTIAL. POTENTIAL). N-LINEED (GLCNAC) (POTENTIAL). N-LINEED (GLCNAC	MAJOR ENVELOPE PROTEIN E (POTENTIAL). NONSTRUCTURAL PROTEIN NS1 (POTENTIAL). NONSTRUCTURAL, DROTREIN NS2 (POTENTIAL).

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22300,
229001;
229001;
220; IPR00031; Cys Ser_trypsin.
220; IPR001410; DEAD.
220; IPR001421; HCV_core.
220; IPR002512; HCV_core.
220; IPR002513; HCV_NS1.
220; IPR002513; HCV_NS1.
220; IPR002513; HCV_NS4.
220; IPR001490; HCV_NS4.
220; IPR001490; HCV_NS4.
220; IPR001490; Peptidase_C29.
220; IPR001490; Peptidase_C29.
220; IPR007095; RNA_pol_DS_PS.
220; IPR007096; HCV_NS1; 1.
220; IPR007096; HCV_NS1; 1.
220; IPR007098; IPR0070
Core protein; C
Transmembrane;
INIT_MET 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genotypes.";
Virology 188:331-341(1992)
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PIR; A40250; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. and NS5 may play a role in the viral RNA replication. CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viprecursor polyprotein, commonly with Asp or Glu in the P6 position. Ys or Thr in P1 and Ser or Ala in P1.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein C and mRNA.
SIMILARITY: THE PROTEASE BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex protein C and mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins:
        protein; Glycoprotein; Transferase; RNA-directed RNA polymerase; protein; Coat protein; Envelope protein; Helicase; ATP-binding; protein; Hydrolase; Serine protease. smembrane; Nonstructural protein, Hydrolase; Serine protease. MET
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NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL)
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Mammalia; Eutheria; Rodentia;
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SUBUNIT: DNA polymerase alpha-primase is a four su (subunits A, B, C and D), which is assembled throw (subunits A) has DNA polymerase alpha-primase by has DNA polymerase alpha-primase is a four su (subunits A) has DNA polymerase alpha-primase is a four su (subunits A) has DNA polymerase alpha-primase is a four su (subunits A) has DNA polymerase alpha-primase is a four su (subunits A) has DNA polymerase alpha-primase is a four su (subunits A) has DNA polymerase alpha-primase is a four su (subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase is a four subunits A) has DNA polymerase alpha-primase alpha-prim
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PTM: PHOSPHORYLATED IN A CELL CYCLE-DEPENDENT MANNER, PHASE (BY SIMILARITY).
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       Ul-AUG-1992 (Rel.; 01-AUG-1992 (Rel.; 10-OCT-2003 (Rel. 4 Serotransferrin prebinding globulin).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=93277958; PubMed=8504171;
Carpenter M.A., Broad T.E.;
"The cDNA sequence of horse transferrin.";
"The cDNA sequence of large transferrin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced th between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McDowell K.J., Adams M.H., Baker C.B.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.

FUNCTION: Transferring are iron binding transport protein can bind two atoms of ferric iron in association with the of an anion, usually bicarbonate. It is responsible for transport of iron from sites of absorption and hame degrathose of storage and utilization. Serum transferrin may a further role in stimulating cell proliferation.

SUBCELLULAR LOCATION: Secreted.

TISSUE SPECIFICITY: Expressed by the liver and secreted in the content of the co
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EMBL; U21127; AAA63684.1; -.
PIR; S33761; S33761.
HSSP; P02787; IABE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: Composed of two homologous domains. SIMILARITY: Belongs to the transferrin family.
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eria; Perissodactyla; Equidae; Equus.
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RT "Hepat.;
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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE Structural protein 2 precursor (ORF2).
S Hepatitis E virus (strain Burma) (HEV).
C Viruses; ssRNA positive-strand viruses, no DNA structural protein 2 precursor (Ref).
C North Structural (HEV).
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MEDLINE=92024067; PubMed=1926770;

Tam A.W., Smith M.M., Guerra M.E.,

Fry K.E., Reyes G.R.;

"Hepatitis E virus (HEV): molecula:
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Best Local S
Matches 72
                                          u1-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Pakistan) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA
Hepatitis E-like viruses.
NCBI TaxID-33774;
                                                                                                                                                    VST2 HEVPA
P33426;
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SIGNAL
CHAIN
SEQUENCE FROM N.A. MEDLINE=92115700; Tsarev S.A., Emers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                full-length viral genome.";
virology 185:120-131(1991).
-:- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RI
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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PIR; C40778; VHWWH2
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or send an email to license@isb-sib.ch).
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InterPro; IPR008975; Viral_cap_coat.
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72; Conserv
                                                                                                                                                                                                                                 NVATGAQAVARSLDWTKV
                                                                                                                                                                                                                                                           RAAVCTRGVAKAVDFIPV
                                                                                                                                                                                                                                                                                DNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYV--SDSVTLV
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                                                                                                                                                                  STANDARD;
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660
70978 MW;
PubMed=1731327;
son S.U., Reyes
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Pred. No. 2.8;
47; Mismatches
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STRUCTURAL PROTEIN
5832A013CCC4A61C
                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                  -TCVNGV-----CWTVFH----
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2.8;
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CRC64;
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Tsareva

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Legters

STANDORD COCCOCCOCCATA

3

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JSULT 13

TPV MOUSE

ID FIPV MOUSE

ID FIPV MOUSE

ID FIPV MOUSE

ID T15-UTL-1998 (Rel. 36, Created)

DT 15-UTL-1998 (Rel. 36, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Receptor-type protein-tyrosine phosphatase V precursor (EC '~mbryonic stem cell protein-tyrosine phosphatase) (ES cel '~mbryonic stem cell protein-tyrosine phosphatase) (ES cel 'Ambryonic stem cell protein-tyrosine phosphatase)
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Best Local &
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malik I.A., Iqbal M., Purcell R.H.;
"Characterization of a prototype strain of hepatitis E virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
-i- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RN
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090; [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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23
660 AA;
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19.0%;
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Pred. No. 2
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STRUCTURAL PROTEIN
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ced. No. 2.8;
Mismatches 11
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74
89
117
174
239
259
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Lee K., Nichols J., Smith A.;

Mech. Dev. 61:213-215(1996).

-i- FUNCTION: May play a role in the maintenance of pluripotency.

Down-regulated during differentiation.

-i- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryonic stem cells;
MEDLINE=97109513; PubMed=8951793;
Lee K., Nichols J., Smith A.;
"Identification of a developmentally regulated protein tyrosine phosphatase in embryonic stem cells that is a marker of pluripotential epiblast and early mesoderm.";
Mech. Dev. 59:153-164(1996).
                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                          tyrosine + phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
DEVELOPMENTAL STAGE: Detectable in the epiblast
throughout early mouse embryo development. In ad
localized in gonadal germ cells.
SIMILARITY: Contains 2 protein-tyrosine phosphat
SIMILARITY: Contains 10 fibronectin type III.don
                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
LYFO
                        AAC52868.1; -.
                                                                                                         noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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e III domains.
                                                                                                                                                                                                                                                                                                                                                                                             adult,
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Th
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Pfam; PF00041; fn3; 7.
Pfam; PF00102; Y phosphatase; 1.
PRANTS; PR00700; PRIYPHPHTASE.
SMART; SM00060; FN3; 8.
SMART; SM00060; FN3; 8.
SMART; SM00194; PTPC; 1.
SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR PHOSPHATASE
PROSITE; PS00383; TYR PHOSPHATASE
PROSITE; PS00383; TYR PHOSPHATASE
PROSITE; PS50055; TYR PHOSPHATASE InterPro; IPR008957; FN III-like. InterPro; IPR003961; FN III. InterPro; IPR000387; TYR phosphatase. InterPro; IPR000242; Tyr_PP. MGD; MGI:108027; Transmembrane; Ptprv. TYR_PHOSPHATASE_1; 1.

TYR_PHOSPHATASE_2; 1.

TYR_PHOSPHATASE_PIP; 2. 1705 1100 1705 199 288 373 454 454 543 634 543 634 1722 813 905 1418 1077 74 89 117 174 239 259 CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 5.

FIBRONECTIN TYPE-III 5.

FIBRONECTIN TYPE-III 6.

FIBRONECTIN TYPE-III 7.

FIBRONECTIN TYPE-III 8.

FIBRONECTIN TYPE-III 9.

FIBRONECTIN TYPE-III 9.

FIBRONECTIN TYPE-III 9.

FIBRONECTIN TYPE-III 10.

PROTEIN-TYROSINE PHOSPHATASE 1.

PROTEIN-TYROSINE PHOSPHATASE 2.

PHOSPHOCYSTEINE INTERMEDIATE (E N-LINKED N-LINKED N-LINKED N-LINKED PHOSPHATASE V. EXTRACELLULAR POTENTIAL. N-LINKED SIMILARITY RECEPTOR-TYPE eat; Signal; Glycoprotein. (GLCNAC. (GLCNAC. (GLCNAC. PROTEIN-TYROSINE (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL) (POTENTIAL) 1. 2. (BY

(GLCNAC.

PTPV MC ID PT PV AC ID PT PV AC PT A

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RESULT 14

VST2 HEVME STANDARD; PRT; 659 AA

ID VST2 HEVME STANDARD; PRT; 659 AA

AC Q0350;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation updat

DE Structural protein 2 precursor.
OS Hepatitis E virus (strain Mexico) (HEV).

OC Viruses; ssRNA positive-strand viruses, no
OC Hepatitis E-1ike viruses.
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Best Local S
Matches 83
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CARBOHYD
       the Europuse by modified
                                                                       VITOLOGY 191:550-558(1992).

-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGITHAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENC
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                            Huang C.C., Nguyen D., Fernandez J., Bradley D.W., Tam A.W., Reyes G.R.; "Molecular cloning and sequencing of
                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=93079857; PubMed=1448913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                   virus (HEV)."
               ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTPLWNELWASWKAGQGARDGYVLKLSGPVE---
                                                                                                                                                                                                                                                                                                                                                         GFAHQPATLRAS--WCHPP-GGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPPQSLEIISRNSPSDLTIGWAPAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSVDAPGLIGNISVSSGATHVTFCGLVPGAHYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DKNOVEGEVOVVSTATOSFLATCVNGVCWTVFHGAGSKTLAGPKGPITOMYT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTPLQD--WAH----AGLRD-----LAVAVEPVIFSDMEVKIITWGADTAACGDIISG--
                                                                                                                                                                                                                                                                                                                                                                                                     PGDLVDLGPDISSLTLKSLVPGSC---YTVSAWAWSGNLSSDSQKIHSCTRPAPPTNLSL
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                                                                                                                                                                                                                                                                                                                                                                                                                           -GSILSPRP-VSYLKGSSGGPLLCPSGHAVGIF-----
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        statement is not removed.
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431
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737
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970
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1; Mismatches
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Pred. No. 1
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                                                                                                                               of the
                                                                                                                                                    Yun K.Y.,
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(GLCNAC.
(GLCNAC.
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                                                                                    ACID CONTENT SUGGESTING IDATION OF THE GENOMIC RNA
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        Usage
                                                                                                                                                                                                                        stage;
                                                                                                                                                    Fry K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1705;
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        and
                                                                                                                                 of hepatitis
is is
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Matches
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Best Local
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SEQUENCE
                                                                                                                                                                                        POLIG_TBEWW STANDARD; PRT; 3414 AA.

P14336; Q88493;
01-JAN-1990 (Rel. 13, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Genome polyprotein (Contains: Capsid protein C (Core protein); Matrix
protein (Envelope protein M); Major envelope protein E, Nonstructural
proteins NS1, NS2B, NS4A and NS4B; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
(NS5)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B44212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M74506; AAA45732.1;
                       encephalitis virus.";
Virology 213:169-178(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03014; SP2; 1.
                                              Wallner G., Mandi C.W., Kunz C., Heinz F.X.;
"The flavivirus 3'-noncoding region: extensive sindependent of evolutionary relationships among
                                                                                     MEDLINE=96036491;
                                                                                                    STRAIN=Neudoerf]
                                                                                                                                                               Viruses; ssRNA positive-strand
                                                                                                                                                                              Tick-borne
                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                       NCBI_TaxID=11088;
                                                                                                                                                      lavivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
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ဝူ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQGL I RACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVZPV
                                                                                                                                                                                                                                                                                                                                                                        VATGAQAVARSLDWSKVTLDGRPLPTVEQYSKT
                                                                                                                                                                                                                                                                                                                                                                                                  AAVCTRGVAKAVDFI-----PVESMETTMRT 319
                                                                                                                                                                                                                                                                                                                                                                                                                         NQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYI--SDSVTLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSAGGQLFYSRPVVSANGEPTVKLYTSVENA----QQDKGVAIPHDIDLGDSRVVIQDYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHSARGADGTAELTTTAATRFMKDLHFTGLNGVGEVGRGIALTLLNLADTLLGGLPTELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --DKNQVEGEVQVVSTATQSFLA----TCVNGV-----CWTVFHGAGSKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRHADVIPVRRRGDSRG-SLLSPRPVSYLK------GSSGGPLLCPSGHAVGIFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
23
659
                                                                                                                                                                              encephalitis virus
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659
70640 MW;
                                                                        PubMed=7483260;
C.W., Kunz C., 1
                                                                                                                 AND REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURAL PROTEIN; CF75E75EFD8FBE2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                  (Western subtype)
d viruses, no DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                            534
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                                                                size
                                                                                                                                                                   stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - PSERLHYRNQGWRSVETSGVA
                                                                                                                                                        (TBEV).
<tage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                   heterogeneity
ains of tick-borne
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InterPro; IPR003003; Cys_Ser_trypsin.
InterPro; IPR001410; DEAD.
InterPro; IPR001122; Flavi_capsidC.
InterPro; IPR001123; Flavi_glycoprotE.
InterPro; IPR0000336; Flavi_M.
InterPro; IPR000069; Flavi_NS2A.
InterPro; IPR0001157; Flavi_NS2A.
InterPro; IPR000157; Flavi_NS2A.
InterPro; IPR000404; Flavi_NS4B.
InterPro; IPR000404; Flavi_NS4B.
InterPro; IPR000404; Flavi_NS4B.
InterPro; IPR001528; Flavi_NS5.
InterPro; IPR001535; Flavi_Dropep.
InterPro; IPR001535; Flavi_Dropep.
InterPro; IPR001535; Flavi_Dropep.
InterPro; IPR001536; Helicase C.
InterPro; IPR007110; Ig-1ike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U27495; AAA86870
PIR; A31052; GNWVNE.
PDB; 1SVB; 10-JUN-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 375:291-298(1995).

-!- FUNCTION: The small proteins NS2A, NS2A, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3 and NS5 may play a role in the viral RNA replication.
-!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N).
-!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
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MEDLINE=95272700; PubMed=7753193;
Rey F.A., Heinz F.X., Mandl C.W., Kunz C., Harrison S.C.;
"The envelope glycoprotein from tick-borne encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mandl C.W., Heinz F.X., Stoeckl E., Kunz C.; "Genome sequence of tick-borne encephalitis virus (Western subtype) and comparative analysis of nonstructural proteins with other
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MEDLINE=8332870; PubMed=3413985;
Mandl C.W., Heinz F.X., Kunz C.;
Mandl C.W., Heinz F.X., Kunz C.;
"Sequence of the structural proteins of tick-borne encephalitis virus
(western subtype) and comparative analysis with other flaviviruses.";
Virology 166:197-205(1988).
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Mandl C.W., Heinz F.X., Stoeckl E
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erPro; IPR001850; Peptidase S7.
erPro; IPR007095; RNA DOL DS PS.
erPro; IPR007094; RNA DOL DS PSVir.
erPro; IPR007094; RNA DOL PSVir.
erPro; IPR007877; RTmJ FtsJ.
m; PF01003; Plavi capsīd; 1.
m; PF01004; Plavi glycoprot; 1.
m; PF01004; Flavi M: 1.
m; PF01005; Flavi M: 1.
m; PF01005; Flavi M: 3.
m; PF01005; Flavi M: 3.
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Pfam; PF01350; Flavi NS4A; 1.

Pfam; PF01349; Flavi NS54, 1.

R Pfam; PF01349; Flavi NS5 1.

R Pfam; PF01570; Flavi Pf050; 1.

R Pfam; PF01570; Flavi Pf060; 1.

R Pfam; PF01728; Ftsy; 1.

R Pfam; PF00171; helicase C; 1.

R Pfam; PF00271; helicase C; 1.

R ProDom; PD001456; Flavi S1; 1.

R ProDom; PD001456; Flavi NS1; 1.

R ProDom; PM001496; Flavi NS1; 1.

R PRODom; SM00490; HELICC; 1.

R SMART; SM00490; HELICC; 1.

R PROSITE; PS00690; DEAH ATTO HELICASE; FALSE NEG.

R PROSITE; PS00690; DEAH ATTO HELICASE; PROSITE; PS00690; PS00
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WONSTRUCTURAL PROTEIN NS2A.

NONSTRUCTURAL PROTEIN NS2B.

NONSTRUCTURAL PROTEIN NS2B.

PROTEASE/HELICASE (NS3).

PROTEASE/HELICASE (NS3).

NONSTRUCTURAL PROTEIN NS4B.

NONSTRUCTURAL PROTEIN NS4B.

NONSTRUCTURAL PROTEIN NS4B.

RNA-DIRECTED RNA POLYMERASE (
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Score	Match	Length	DB .	ID	Description	
1551	87.6	3010	12	Q9J3H7	Q9i3h7 hepatitis	Ω .
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Q9j3g3	Q81541	Q9qiy4	Q9dte9	Q9qiy5	Q9j3i1	Q8 <u>q</u> r18	Q9j3g6	Q9qp61	070818	Q9dte3	Q99au2	Q9dte0	Q9dtf0	Q9dtd7	P89966	Q68788	281817	081755	Q9j3h4	Q9wmx2	0913h9	Q91au0	.009796	Q9j3h6	Q9qix5	Q9qix6	<u> </u>	Q9qiy7
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

ISOBUNIT: THE VIRLON OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE: THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).

EMBL; AF207756; AAR65946.1; -.

EMBL; A61196; A61196.

PIR; P000246; P00004.

PIR; P000246; P00004.

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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C. "Characteristics of hepatitis C viral genome associated with disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=MD15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome polyprotein.
Hepatitis C virus.
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GO:0016021; C:integral to membrane; IEA.
GO:0019028; C:viral capsid; IEA.
GO:0019028; C:viral envelope; IEA.
GO:0019031; C:viral envelope; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0008026; F:ATP dependent helicase activity; IEA.
GO:0005489; F:electron transporter activity; IEA.
GO:0003723; F:RNA binding; IEA.
GO:0003723; F:RNA-directed RNA polymerase activity;
GO:0008236; F:extine-type peptidase activity; IEA.
GO:0008236; F:structural molecule activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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25,
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Last sequence update)
Last annotation update)
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RESULT 2
Q68826
ID Q688
AC Q688
DT 01-N
DT 01-N
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Best Local S
Matches 290
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Pfam; PR01539; HCV env; 1.
Pfam; PF01560; HCV NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS5a; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF01506; Viral RdRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0019079; P:viral genome replication; IEA.

GO; GO:0019087; P:viral transformation; IEA.

InterPro; IPR009003; Cys Ser_trypsin.

InterPro; IPR009445; CytC heme BS.

InterPro; IPR001410; DEAD.

InterPro; IPR002521; HCV_capsid.

InterPro; IPR002521; HCV_core.

InterPro; IPR002521; HCV_env.

InterPro; IPR002531; HCV_NS1.
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InterPro; IPR0021
InterPro; IPR0041
InterPro; IPR0070
InterPro; IPR0070
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InterPro;
InterPro;
                    Q68826 PRELIMINARY;
Q68826;
Q1-NOV-1996 (Tremetrel. 01,
01-NOV-1996 (Tremetrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00190; CYTOCHROME C; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 327365 MW; D8653F7317FFA106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01543; HCV
Pfam; PF01542; HCV
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GO:0006118;
GO:0006508;
GO:0006350;
GO:0019079;
GO:0019087;
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                                                                                                                                                                                                                                                                      ŔŔĠĎŚŔĠŚĹĹŚPŔPVSYĹKĠŚŚĠĠĎĹĹĆPŚĠHAVGIFRAAVCTRĠVAKAVDFVPVESMET
                                                                                                                                                                                                                                                                                                                                                                          GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                                                                                                                                                                                    GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                                                                                                                                                                                                                                                                                RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
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P:proteolysis and peptidolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P:transcription; IEA.
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HCV_NS1; 1.
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HCV capsid.
HCV core.
HCV env.
HCV_NS1.
HCV_NS4.
HCV_NS4a.
HCV_NS4b.
HCV_NS4b.
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95.4%;
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                       Last sequence update)
                                            Created)
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Pred. No. 4.6e-126;
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                                                                                        3010
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HSSP, P2666; 1JXP.

R GO; GO:0016021; C:viral capsid; IEA.

R GO; GO:0019028; C:viral envelope; IEA.

R GO; GO:0019021; C:viral envelope; IEA.

R GO; GO:0019021; C:viral envelope; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005787; F:ATP dependent helicase activity; IEA.

R GO; GO:0003723; F:RNA-binding; IEA.

R GO; GO:0003723; F:RNA-binding; IEA.

R GO; GO:0003723; F:RNA-binding; IEA.

R GO; GO:0003968; F:RRA-directed RNA polymerase activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0005198; F:transferase activity; IEA.

R GO; GO:0005199; F:transferase activity; IEA.

R GO; GO:0006309; P:transferase activity; IEA.

R GO; GO:0019079; P:viral genome replication; IEA.

R GO; GO:0019087; P:viral transformation; IEA.
Query Match
Best Local Similarity
                                                                                                           InterPro; IPR007094; RNA POL DS
InterPro; IPR007094; RNA POL PS
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01542; HCV core; 1
Pfam; PF01542; HCV env; 1.
Pfam; PF01539; HCV NS1; 1.
Pfam; PF01539; HCV NS2; 1.
Pfam; PF01538; HCV NS3; 1.
Pfam; PF01538; HCV NS3; 1.
Pfam; PF01506; HCV NS4a; 1.
Pfam; PF01001; HCV NS5a; 1.
Pfam; PF01001; HCV NS5a; 1.
Pfam; PF01506; HCV NS5a; 1.
Pfam; PF01506; HCV NS5a; 1.
Pfam; PF00998; Viral RdRP; 1.
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PIR; A61166; A61196.
PIR; PQ0246; PD00246.
PIR; PQ0804; PQ0804.
PIR; PS03229.
PS03229.
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STRAIN=J33;
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NCBI_TaxID=11103;
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Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cho M.J.; "Molecular cloning of Hepatitis C virus genome from a single Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; seRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                Hydrolase, Nonstructural protein; RNA-directed RNA polymerase; Trans SEQUENCE 3010 AA; 327150 MW;
                                                                                                SMART; SM004
ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).
L; D14484; BAA03375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR009003;
                                                                                                                                                                                                                                                                                                                                      PROUZIDO; III. PROUISO, Helicase C.
PROU4109; Peptidase C29.
PROU7095; RNA_pol_pS_PS.
PROU7094; RNA_pol_PSvir.
                                                                                               Coat protein; Envelope protein; Glycoprotein; Helicase;
                                                                                                                                                                                                                                                                                                                                                                                                          131; HCV capsid.
1121; HCV core.
1121; HCV env.
1131; HCV NS1.
118; HCV NS2.
118; HCV NS4a.
1905; HCV NS5a.
166; HCV RdRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cys_Ser_trypsin.
DEAD.
 87.3%;
96.1%;
                                                  tein; Polyprotein;
Transferase; Transmembrane.
MW; 7270F47984554FAD CRC64;
 Score 1546; DB 12;
Pred. No. 1.3e-125;
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                 Length 3010;
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PRESULT

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WA Enomoto N., Sakuma I., Asahina Y., Kurosaki M., Murakami T.,

Yamamoto C., Izumi N., Marumo F., Sato C.;

Yamamoto N., Sato C.;

Yamamoto C., Izumi N., Marumo F., Sato C., No. Sato C., No.
EMBL; D50482; BAA09073.1; -...

R PIR; A61196; A61196.

R PIR; P00254, P00254.

R PIR; P00254, P00804.

R PIR; P00269; P00329.

R PIR; P00804; P00804.

R PIR; P00804; P00804.

R PIR; P00801; C:viral capsid; IEA.

GO; GO:0019021; C:viral envelope; IEA.

GO; GO:0019021; F:ATP binding; IEA.

GO; GO:0019025; F:ATP binding; IEA.

GO; GO:0003123; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003123; F:SENA-directed RNA polymerase activity; IEA.

R GO; GO:0005196; F:SENA-directed RNA polymerase activity; IEA.

R GO; GO:00051976; F:stransferase activity; IEA.

GO; GO:00051976; F:transferase activity; IEA.
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P90191;
01-MAY-1997 (TIEMBLIEL C
01-MAY-1997 (TIEMBLIEL C
01-OCT-2003 (TIEMBLIEL C
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NCBI_TaxID=11103;
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Hepatitis C virus.
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n; PF01539; HCV_env; 1.

n; PF01539; HCV_NS2; 1.

n; PF01538; HCV_NS2; 1.

n; PF01001; HCV_NS3; 1.

n; PF01001; HCV_NS4b; 1.

n; PF01506; HCV_NS4b; 1.

n; PF01506; HCV_NS4b; 1.

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; IPR007095; RNA
; IPR007094; RNA
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IPR001410; DEAD.
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i RNA polymerase; Transferase; Transmembrane.
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01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients with hepatocellular carcinoma: the 'progression score' revisited."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-i-SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB049091; BAB18804.1;
PIR; A61196; A61196.
PIR; PS0329; PS0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9DTE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:001672; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005626; F:ATP bending; IEA.
GO; GO:0006026; F:ATP dependent helicase activity; IEA.
GO; GO:0006787; F:hydrolase activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003968; F:serine-type peptidase activity; IEA.
GO; GO:0005108; F:structural molecule activity; IEA.
GO; GO:0005108; F:stransferase activity; IEA.
GO; GO:0006110; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mishiro S.;
                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                              nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                  nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0006118; P:electron transpo
GO:0006508; P:proteolysis and
GO:0006350; P:transcription; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0019087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P26663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19079; P:viral genome replication; 19087; P:viral transformation; IEA. IPR009003; Cyts Ser trypsin. IPR000345; Cytc heme_BS.
                                                                                                                                                                                                                              IPR004109; Peptidase C29.
IPR007095; RNA pol DS PS.
IPR007094; RNA pol PSvir.
1543; HCV_capsid; 1.
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                         HCV_core; 1.
HCV_env; 1.
HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
HCV_NS4a; 1.
HCV_NS4a; 1.
HCV_NS4b; 1.
HCV_NS5a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JJXP
     helicase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:RNA-directed RNA polymerase activity;
                                                                                                                                                                                                                                                                                                                                                         HCV_NS4b.
HCV_NS5a.
HCV_RdRP.
                                                                                                                                                                                                                                                                                                                                  Helicase_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptidolysis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEA.
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       DRR REAL COCCOCCE TO THE PROPERTY OF THE PROPE
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Best Local Similarity
Matches 290; Conserv
EMBL; AB049093; BAB18806:1; -
PIR; A61196; A61196.
PIR; PQ0246; PQ0246.
PIR; PQ0204; PQ0804.
PIR; PS0329; PS0329.
HSSP; P26663; 1JXP.
GG; GG:0016021; C:integral to GO; GG:0019028; C:viral capsid GO; GG:0019031; C:viral envelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9DTE4;
Q9DTE4;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00190; CYTOCHROME_C; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein
Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 327042 MW; 3807DC6879684C95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00998; Viral RdRP;
ProDom; PD186062; HCV_NS1;
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi K., Iwata K., Matsumoto M., Matsumoto H.
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HCVT150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    depatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
       GO:0016021; C:integral to membrane; GO:0019028; C:viral capsid; IEA. GO:0019031; C:viral envelope; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1024 RLLAPITAYSQOTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVVDHLTPLQDWAHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>LRDLAVAVEPVVFSDMETKIITWGADTAACGDIISGLPVSARRGREILLGPADSLEGQGW</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGSKTLAGPKGPITOMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virus.
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25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1545;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                            IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Nakao
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1204 TMRS 1207

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R Pfam; PF01543; HCV_core; Nam, Dolfforth.

R Pfam; PF01542; HCV_core; 1.

R Pfam; PF01542; HCV_core; 1.

R Pfam; PF01539; HCV_env; 1.

R Pfam; PF01560; HCV_NS1; 1.

R Pfam; PF01560; HCV_NS4; 1.

R Pfam; PF01006; HCV_NS4a; 1.

R Pfam; PF01006; HCV_NS4a; 1.

R Pfam; PF01001; HCV_NS4a; 1.

R Pfam; PF01001; HCV_NS4a; 1.

R Pfam; PF01006; HCV_NS5a; 1.

R Pfam; PF00271; hellCase C; 1.

R Pfam; PF00271; hellCase C; 1.

R Pfam; PF00998; Viral RdRP; 1.

PR Pfam; PF00998; Viral RdRP; 1.

PR Pfam; PF00099; CYTOCHROME C; 1.

R SMART; SM00487; DEXDC; 1.

R RNGSITE; PS00190; CYTOCHROME C; 1.

R PROSITE; PS00190; CYTOCHROME C; 1.

R PROSITE; PS00190; CYTOCHROME C; 1.

R POLYPOTEEIN; Envelope protein; Glycoprotein; Nonstructural protein; W Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.

SQ SEQUENCE 3010 AA; 327324 MW; 3DE6CF249BD1151C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR009003; Cys Ser Ltypsin.
InterPro; IPR009045; Cyc heme BS.
InterPro; IPR001410; D2AD.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
InterPro; IPR002521; HCV env.
InterPro; IPR002531; HCV NS1.
InterPro; IPR002531; HCV NS2.
InterPro; IPR002518; HCV NS4.
InterPro; IPR001650; HCV NS46.
InterPro; IPR001650; HCV NS46.
InterPro; IPR00165; HCV NS46.
InterPro; IPR00165; HCV NS46.
InterPro; IPR002166; HCV RdRP.
InterPro; IPR001650; Helicase C.
InterPro; IPR001650; Helicase C.
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GG; GG:0008026; F:ATP dependent helicase activity; IEA.
GG; GG:0005489; F:electron transporter activity; IEA.
GG; GG:0003723; F:RNA binding; IEA.
GG; GG:0003723; F:RNA-directed RNA polymerase activity; IEA.
GG; GG:0008236; F:serine-type peptidase activity; IEA.
GG; GG:0008236; F:structural molecule activity; IEA.
GG; GG:0005198; F:structural molecule activity; IEA.
GG; GG:0006508; F:structural molecule activity; IEA.
GG; GG:0006518; P:electron transport; IEA.
GG; GG:0006508; P:proteclysis and peptidolysis; IEA.
GG; GG:0006508; P:transcription; IEA.
GG; GG:0006508; P:transcription; IEA.
GG; GG:0006508; P:transcription; IEA.
GG; GG:0006508; P:transcription; IEA.
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                                                                                                                                           RRGDGRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET
                                                                                                                                                                        RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET 315
                                                                                                                                                                                                                                         RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYH
                                                                                                                                                                                                                                                                                                                                                                               RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
                                                                                                                                                                                                                                                                                                                                                                                                                                            LRDLAVAVEPVVFSDMETKIITWGADTAACGDIILGLPVSARRGKEILLGPADSLEGOGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGITKVPYFVRAQGLIRACMLVRKVAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVVDHLTPLQDWAHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.1%; Score 1543; DB 12; 95.4%; Pred. No. 2.3e-125; tive 8; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3010;
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HSSP, P2663; JAXP,
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; F:ATP dependent helicase activity; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0005737; F:Hydrolase activity; IEA.
GO; GO:0005723; F:RNA binding; IEA.
GO; GO:0005723; F:RNA binding; IEA.
GO; GO:0005723; F:RNA binding; IEA.
GO; GO:0005246; F:Serine-type peptidase activity; IEA.
GO; GO:000518; F:Serine-type peptidase activity; IEA.
GO; GO:0005198; F:Serine-type peptidase activity; IEA.
GO; GO:0005198; F:Serine-type peptidase; IEA.
R GO; GO:0005198; F:Serine-type peptidase; IEA.
R GO; GO:0005198; F:Serine-type peptidase; IEA.
R GO; GO:000523; HCV_Core.
DR InterPro; IPR001419; DEAD.
DR InterPro; IPR002521; HCV_Core.
DR InterPro; IPR002521; HCV_Core.
DR InterPro; IPR002521; HCV_NS4a.
DR InterPro; IPR002511; HCV_NS4a.
DR InterPro; IPR002511; HCV_NS4a.
DR InterPro; IPR00149; HCV_NS4a.
DR InterPro; IPR00155; HcV_NS4a.
DR InterPro; IPR00155; HcV_NS4a.
DR InterPro; IPR00165; HcV_NS4
                                                          "Hepatitis C virus (HCV) genotype 1b sequences from fifteen patient with hepatocellular carcinoma: the 'progression score' revisited.", Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MANA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9DTD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB049101; BAB18814.1; -. 
PIR; A61196; A61196. 
PIR; PQ02446; PQ0246. 
PIR; PS0329; PS0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome polyprotein.
Hepatitis C virus:
Viruses; ssRNA positive-strand
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01-MAR-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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re' revisited.";
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InterPro; IPR004109; Peptidase C29.
InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR007094; RNA pol PSvir.
Pfam; PF01543; HCV_capsid; 1

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TMRT 319

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Query Match Best Local : Matches

l Similarity 95.4 290; Conservative

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Best Local
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Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF00998; Viral_RGRP; 1.
ProDom; PD186062; HCV_NS1; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHAT; SHOUTS; FINDING C; 1.

PROSITE, PS00190; CYTOCHROME C; 1.

ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.

RNA-directed RNA polymerase; MM; DE182D810EF78EE4 CRC64;
                      Enomoto N., Sakuma I., Asahina Y., Kurosaki M., Murakami T., Yamamoto C., Izumi N., Marumo F., Sato C.;
"Comparison of full-length sequences of interferon-sensitive and resistant hepatitis C virus 1b.";
J. Clin. Invest. 96:224-230(1995).
J. Clin. Invest. 96:224-230(1995).
LIBOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN MAND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MENA (BY SIMILARITY).

EMBL; D50484; BAA09075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P88803;
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Hepatitis C virus.
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01-MAY-1997 (TrEMBLrel. 03,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                   STRAIN=HCV-1b;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  RITOMOTO
                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P88803
                                                                                                                                                                                MEDLINE=95340824; PubMed=7542279;
                                                                                                                                                                                                                                               Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 RILAPITAYSOCTRGLIGCIITSLIGRDKNOVEGEVOVVSTATOSFLATCVNGVCWTVFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RILAPITAYSQQTRGLLGCIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.1%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Last annotation update)
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Pred. No. 2.8e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 3010 AA
                                                                                                                                                                                                                                                                                                                                                         viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                         DNA stage; Flaviviridae;
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R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:00019031; C:viral envelope; IEA.

R GO; GO:0008524; F:ATP binding; IEA.

R GO; GO:0008256; F:ATP dependent helicase activity; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003968; F:structural molecule activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006508; P:transcription; IEA.

R GO; GO:0006509; P:viral transformation; IEA.

R GO; GO:0019087; P:viral transformation; IEA.
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Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF02907; HCV_NS2; 1.
Pfam; PF02907; HCV_NS43; 1.
Pfam; PF01006; HCV_NS43; 1.
Pfam; PF01001; HCV_NS40; 1.
Pfam; PF01506; HCV_NS40; 1.
Pfam; PF01506; HCV_NS40; 1.
Pfam; PF01506; HCV_NS40; 1.
Pfam; PF00271; helicase C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polyprotein; I CHAIN CHAIN 11 CHAIN 31 CHAIN 31 CHAIN 10: CHAIN 10: CHAIN 11: CHAIN 11: CHAIN 11: CHAIN 124 CHAIN 129 CHAIN 19 CHAIN 19 CHAIN 19 CHAIN 19 CHAIN 19 CHAIN 30
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InterPro;
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196 GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 255
                                                                                                                                                                                                                                                                                                                                          904
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O; IPR002521; HCV_core.

O; IPR002521; HCV_env.

O; IPR002519; HCV_MS1.

IPR002531; HCV_NS1.

IPR002531; HCV_NS3.

IPR00254; HCV_NS4a.

IPR002166; HCV_NS4b.

IPR002166; HCV_NS6B.

IPR002166; HCV_NS6B.

IPR004109; Peptidase_C.

IPR004109; Peptidase_C.

IPR007094; RNA_pol_DS_PS.

IPR007095; RNA_pol_DS_PS.

IPR007095; RNA_pol_DS_PS.

IPR007095; RNA_pol_DS_PS.

IPR007096; RNA_pol_DS_PS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                     RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
                                                                                                                                                                                                                                            LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW
                                                                                                                                                                                                                                                                                                                                                                                                        AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
                                                                 RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
                                                                                                                                                                                                    LRDLAVAVEPVVFSDMETKI ITWGADTAACGDI ISGLPVSARRGREILLGPADSFEGQGW
                                                                                                                                                                                                                                                                                                                                       AGLIRVPYFVRAQGLIRVCMLVRKVAGGHYVQMAFVKLAALTGTYVYNHLTPLQDWAHTG
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IPR001410; DEAD.
IPR002522; HCV_capsid.
IPR002521; HCV_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
810
1027
1658
1712
1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               () Envelope protein; Glycoprotein; Nonstructural protein; RNA-directed RNA polymerase; Transferase; Transmembrane 192 383 E1 202 NS2. 1657 NS3. 1658 1711 NS4B. 1973 NS4B. 1973 NS5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
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95.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1541;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5F81505783FEFFB8 CRC64;
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DR PIR; A61196; A61196.

DR PIR; PQ0246; PQ0246.

DR PIR; PQ0244; PQ0254.

DR PIR; PG0329; PS0329.

DR HSSP; P27958; 1HEI.

DR GO; GO:0015021; C:viral capsid; IE.

GO; GO:0015021; C:viral capsid; IE.

GO; GO:0005524; F:ATP dependent he:

GO; GO:0005524; F:ATP dependent he:

GO; GO:0005524; F:ATP dependent he:

GO; GO:0005787; F:hydrolase activit

GO; GO:0005787; F:hydrolase activit

GO; GO:0005198; F:ELECTION transport

GO; GO:0005198; F:ELECTION transport

GO; GO:0005198; F:ELECTION transport

GO; GO:0005198; F:ETRINA binding; IEA.

R GO; GO:0005198; F:ETRINA directed RNA

GO; GO:0005198; F:ETRINA directed RNA

R GO; GO:0005198; F:ETRINA directed RNA

InterPro; IPR002511; HCV Capsid.

InterPro; IPR002512; HCV Capsid.

InterPro; IPR002513; HCV NS4a.

InterPro; IPR002166; HCV RdRP.

InterPro; IPR002166; HCV RdRP.
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Q9J3H5;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagayama K., Kurc "Characteristics progression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005529; F:ATP binding; IEA.
GO; GO:000549; F:Hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:transferase activity; IEA.
GO; GO:0006508; P:transferase activity; IEA.
GO; GO:0006508; P:transcription; IEA.
GO; GO:0006508; P:transcription; IEA.
GO; GO:0006350; P:transcription; IEA.
GO; GO:0006350; P:transcription; IEA.
GO; GO:0006397; P:viral genome replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome polyprotein. Hepatitis C virus.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MENA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:RNA-directed RNA polymerase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P:viral genome replicat:
P:viral transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication; IEA ormation; IEA.
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annotation
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on update)
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disease
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                            RESULT ID OF PROPERTY OF PROPE
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Pfam; PR01542; HCV core; 1.

Pfam; PR01542; HCV core; 1.

Pfam; PR01539; HCV env; 1.

Pfam; PR01539; HCV NS1; 1.

Pfam; PR01560; HCV NS2; 1.

Pfam; PR01006; HCV NS4a; 1.

Pfam; PR01001; HCV NS4a; 1.

Pfam; PR01001; HCV NS4b; 1.

Pfam; PR01566; HCV NS4a; 1.

Pfam; PR01566; HCV NS4b; 1.

Pfam; PR01566; HCV NS4b; 1.

Pfam; PR01566; HCV NS4b; 1.

Pfam; PR015662; HCV NS5a; 1.

R Pfam; PR015667; DEXDC; 1.

R Pfam; PR015667; DEXDC; 1.

R PROSITE; PS00190; COTTOCHROME C; 1.

RNART; SM00487; DEXDC; 1.

RN PROSITE; PS00190; COTTOCHROME C; 1.

RN PROSITE; PS00190; COTTOCHROME C; 1.

RW Hydrolase; Nonstructural protein; Glycoprotein; Heli

KW Hydrolase; Nonstructural protein; Polyprotein;

KW RNA-directed RNA polymerase; Transferase; Transmembrane.

SEQUENCE 3010 AA; 326801 MW; 9FEE3D1B93B7AA4B CRC64;

SEQUENCE 1540; DB 12; Length 3010
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                         MEDLINE=22047193; PubMed=12051758;
Kishine H., Sugiyama K., Hijikata M., Kato N., T
Nio Y.; Hosaka M., Miyanari Y., Shimotohno K.;
"Subgenomic replicon derived from a cell line in
hepatitis C virus.";
Biochem. Biophys. Res. Commun. 293:993-999(2002)
EMBL; AB080299; BAC54896.1;
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
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01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                           Polyprotein.
Hepatitis C virus.
Viruses; asRNA positive-strand
                                                                                                                                                                                                                                                                                                  STRAIN-M1LE;
                                                                                                                                                                                                                                                                                                                                                                                                                        Hepacivirus
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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annotation update)
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195

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135

963 75 0

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Gaps

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J336; F.

J5198; F. Structu...

O6118; P. Selectron transpo-
J06508; P. Sproteolysis and Deptido...

J06508; P. Stranscription; IEA.

O019079; P. Viral genome replication; IEA.

O019087; P. Viral genome replication; IEA.

Pro; IPR000345; CytC heme_BS.

Pro; IPR000345; CytC heme_BS.

Pro; IPR000345; CytC heme_BS.

Pro; IPR002522; HCV_Capsid.

APPro; IPR002523; HCV_NS1.

APPro; IPR002523; HCV_NS1.

APPro; IPR002523; HCV_NS4A.

INTERPRO; IPR002519; HCV_NS4A.

INTERPRO; IPR002519; HCV_NS4A.

INTERPRO; IPR002519; HCV_NS4A.

INTERPRO; IPR002519; HCV_NS4A.

INTERPRO; IPR002166; HCV_NS4A.

INTERPRO; IPR007095; RNA_DOL_PSVir.

Pfam; PF01543; HCV_Capsid; 1.

DR Pfam; PF01553; HCV_Capsid; 1.

DR Pfam; PF01553; HCV_Capsid; 1.

DR Pfam; PF01558; HCV_NS3; 1.

DR Pfam; PF01566; HCV_NS3; 1.

DR Pfam; PF01006; HCV_NS3; 1.

DR Pfam; PF00271; helicase_C; 1.

DR Pfam; PF00998; Viral RdRP; 1.

DR Pfam; PF00998; Viral RdRP; 1.

DR Pfam; PF01666; HCV_NS1; 1.

DR Pfam; Pf0166; HCV_NS1; 1.

DR Pfam; Pf0
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Best Local Sim
Matches 291;
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GO: 0005489
GO: 0003723
GO: 0003968
GO: 0005188
GO: 0005198
GO: 0005118
GO: 0006518
GO: 0006598
GO: 0006598
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                                                                                                                                                  RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                          GAGSKTLAGPKGPITOMYTNVDODLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>LRDLAVAVEPVVFSDMETKIITWGADTAACGDIILGLPVSARRGREILLGPADSLEGQGW</u>
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TMRS 1207
                                                        TMRT
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16; F:ATP dependent helicase activity; IEA.
19; F:electron transporter activity; IEA.
13; F:RNA binding; IEA.
13; F:RNA-directed RNA polymerase activity; IEA.
16; F:serine-type peptidase activity; IEA.
18; F:structural molecule activity; IEA.
18; P:electron transport; IEA.
18; P:electron transport; IEA.
18; P:proteolysis and peptidolysis; IEA.
                                                     319
                                                                                                                   LLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1540; DB 12;
Pred. No. 4.2e-125;
6; Mismatches 7;
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RESULT 10
Q9J3F9
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REMBI, A61196, A61196.

PIR; A61196, P60246.

PIR; P80329; P80329; P80329.

REMBI, P
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Q9J3F9;
01-OCT-2000
                    InterPro;
Pfam; Pro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
InterPro;
InterPro;
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submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
1. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY
1. LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MENA (BY SIMILARITY).
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01-OCT-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
InterPro;
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NCBI_TaxID=11103;
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Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome polyprotein.
Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [nterPro;
GC:001090350; P:transcription; IEA.
GC:00109079; P:viral genome replication; IEA.
GC:0019087; P:viral transformation; I
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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Best Local Sim
Matches 288;
EMML; ADULTUTE AND TRANSP; P27958; HEI.
HSSP; P27958; HEI.
GO; GO:0008236; F:Serine-type peptidase activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
GO; GO:0019067; P:viral transformation; IEA.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR009518; HCV_NS2.
InterPro; IPR004109; PepTidase_C29.
Pfam; PP01538; HCV_NS2; 1.
                                                                                                                                                        "Enzymatic characterization on hepatitis C virus expressed in FEBS Lett. 378:37-42(1998).

EMBL, AB013620; BAA28498.1; -
HSSP; P27958; 1HEI.
GC; GC:0008236; F:Serine-type GC; GC:0006508; P:proteolysis GO; GO:0019087; P:viral transformation of the company of the
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070815;
01-AUG-1998
01-AUG-1998
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada K., No.
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Pfam; PF00998; Viral RdRP; 1.
Probom; PD186062; HCV NS1; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; CYTOCHROME C; 1.
PROSITE; PS001190; CYTOCHROME C; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural Polyprotein; RNA-directed RNA polymerase; Transferase; Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98321154; PubMed=9656998; MEDLINE-98321154; PubMed=9656998; Medline-worl A., Seki M., Kimu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyprotein (Fragment).
Hepatitis C virus.
Viruses; seRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyamura T
"Enzymatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mori A.,
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Virology 246:104-112(1998).
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Yamada K.,
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                      TMRT
                                                          RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                            RRGDSRGSLLSPRPISYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                           GAGSKTLAGPKGPVTQMYTNVDLDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVR
                                                                                                           GAGSKTLAGÞKGÞITQMYTNVDQDLVGWQAÞÞGARSMTÞCTCGSSBLYLVTRHADVIÞVR
                                                                                                                                        RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWSVYH
                                                                                                                                                                                       LRDLAVAVEPVVFSDMETKIITWGADTAACGDIISGLPVSARRGREVLLGPADSFEHQGW
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                                                                                                                                                                                                                                                                                                                               361
361 AA;
                                                                                                                                                                                                                                                                                  Conservative
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38336 MW;
                                                                                                                                                                                                                                                                                            86.7%; Score 1535; DB 12; 94.7%; Pred. No. 7.1e-126;
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RESULT OF STREET OF STREET
R EMBL; AF208024; AAR61205.1; -..

R PIR; A61196; A61196.

R PIR; P302246; P00246.

R PIR; P30229; P30329.

R HSSP; P36663; JJXP.

R GO; GO:0016021; C:viral capsid; IEA.

R GO; GO:0019021; C:viral envelope; IEA.

R GO; GO:0019021; C:viral envelope; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:00005524; F:ATP dependent helicase activity; IEA.

R GO; GO:0008126; F:ATP dependent helicase activity; IEA.

R GO; GO:0008128; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003956; F:SRA-directed RNA polymerase activity; IEA.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Submitted (1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MD34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECARSID COVERED
LIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLECCAPSID IS A COMPLEX
PROTEIN C AND MRNA (BY SIMILARITY).
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annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stage; Flaviviridae;
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disease

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RESULT 13
Q9J3H3
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InterPro; 1PR002521; HCV_core.

InterPro; 1PR002521; HCV_core.

InterPro; 1PR002519; HCV_env.

InterPro; 1PR002519; HCV_NS2.

InterPro; 1PR002518; HCV_NS2.

InterPro; 1PR002518; HCV_NS3.

InterPro; 1PR001490; HCV_NS44.

InterPro; 1PR001491; HCV_NS54.

InterPro; 1PR001650; HCV_NS54.

InterPro; 1PR001650; HCV_NS54.

InterPro; 1PR001650; HCV_NS54.

InterPro; 1PR007094; RNA_pol_PSVIr.

Pfam; PF01542; HCV_capsid; 1.

Pfam; PF01542; HCV_capsid; 1.

Pfam; PF01542; HCV_NS1; 1.

Pfam; PF01542; HCV_NS1; 1.

Pfam; PF01543; HCV_NS2; 1.

Pfam; PF01543; HCV_NS2; 1.

Pfam; PF01542; HCV_NS2; 1.

Pfam; PF01543; HCV_NS3; 1.

Pfam; PF01543; HCV_NS4; 1.

Pfam; PF01543; HCV_NS4; 1.

Pfam; PF0156; HCV_NS4; 1.

Pfam; PF01001; HCV_NS4; 1.

Pfam; PF010038; V1ral_RdRP; 1.

Pfam; PF00398; V1ral_RdRP; 1.

Pfam; PF00398; V1ral_RdRP; 1.

Pfam; PF00304; DEND; 1.

Pfam; PF0154; DCD_LT, 1.

PR Pfam; PF0154; DCD_LT, 1.

PR Pfam; PF0154; DCD_LT, 1.

Pfam; PF0154; HCV_NS4; 1.

Pfam; PF0154; DCD_LT, 1.

Pfam; PF0156; HCV_NS4; 1.

Pfam; PF0156; HCV_NS4; 1.

Pfam; PF0156; HCV_NS4; 1.

Pfam; PF0157; DEND; 1.

Pfam; PF0156; HCV_NS4; 1.

Pfa
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Best Local S
Matches 290
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InterPro;
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GO:0006740;
GO:0006118;
GO:0006508;
GO:0006350;
GO:0019079;
GO:0019087;
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                                                                                                                                                                                                                                                                                                                                                                                       GAGSKTLAGÞKGÞÍTÓMYTNVÞÓÐLVGWÓÁÞÞGARSLTÞCTCGSSÐLYLVTRHAÐVÍÞVR
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IPR000345; CytC heme_BS.
IPR001410; DEAD.
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P:viral transformation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:structural molecule activity; IEA.
F:transferase activity; IEA.
P:electron transport; IEA.
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Pred. No. 1
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InterPro; IPRO0150; Helicase_C.

R InterPro; IPR00160; Peptidase_C.

R InterPro; IPR007094; RNA_pol_DS_PS.

InterPro; IPR007094; RNA_pol_DS_PS.

R InterPro; IPR007094; RNA_pol_DS_PS.

R InterPro; IPR007094; RNA_pol_PSVir.

Pfam; PF01543; HCV_core; 1.

Pfam; PF01542; HCV_core; 1.

Pfam; PF01559; HCV_NS2; 1.

Pfam; PF01560; HCV_NS2; 1.

R Pfam; PF01006; HCV_NS3; 1.

R Pfam; PF01006; HCV_NS4; 1.

R Pfam; PF01006; HCV_NS4; 1.

Pfam; PF01006; HCV_NS4; 1.

R Pfam; PF01071; Helicase_C; 1.

Pfam; PF01071; Helicase_C; 1.

Pfam; PF00998; Viral_RdEP; 1.

R Pfam; PF00998; Viral_RdEP; 1.

R Pfam; PF016062; HCV_NS1; 1.

R Pfam; PF016062; HCV_NS1; 1.

R PROSITE; PS00190; CYTOCHROME_C; 1.

R SMART; SM00487; DEXDC; 1.

R SMART; SM00487; DEXDC; 1.

R SMART; SM00487; DEXDC; 1.

R SMART; SM00487; RNA-directed RNA polymerase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016021; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000526; F:ATP binding; IEA.
GO; GO:000373; F:RNA binding; IEA.
GO; GO:000373; F:RNA binding; IEA.
GO; GO:000373; F:RNA directed RNA polymerase activity; IEA.
GO; GO:000356; F:serine-type peptidase activity; IEA.
GO; GO:0005196; F:structural molecule activity; IEA.
GO; GO:0005196; F:structural molecule activity; IEA.
GO; GO:0005196; F:structural molecule activity; IEA.
GO; GO:00065196; P:protectysis and peptidolysis; IEA.
GO; GO:0006508; P:protectysis and peptidolysis; IEA.
GO; GO:0006508; P:transcription; IEA.
GO; GO:0006509; P:viral transformation; IEA.
GO; GO:0006509; P:viral transformation; IEA.
InterPro; IPR003003; Cys_Ser_trypsin.
InterPro; IPR003045; CytC_heme_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
InterPro;
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9J3H3, PRELIMINARY;
Q9J3H3, 01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF207760; AAF65950.1; -. PIR; A61196; A61196. PIR; PS0329; PS0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           progression."
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NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MD19;
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                                                                                                                                                                                                                                                                                                                                             nterPro;
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCARSID COVERED BY
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA, (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P26663;
                                                                                                                                                                                                                                                                                                          IPRO01410; DÉAD.

IPRO02522; HCV capsid.

IPRO02521; HCV core.

IPRO02519; HCV env.

IPRO02518; HCV NS1.

IPRO02531; HCV NS2.

IPRO02531; HCV NS4b.

IPRO01490; HCV NS4b.

IPRO01666; HCV NS4b.

IPRO01666; HCV RdRP.

IPRO01650; Helicase C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Best Local 9
                   Q9J3H2;
Q9J3H2;
01-OCT-2000
                                                                                                                                                                           Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-:- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA (BY SIMILARITY).
EMBL; AF207761; AAF65951.1; -.
EMBL; A61196; A61196.
FIR; P00246; P00246.
FIR; P00329; P50329.
                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                       progression.";
                                                                                                                                                                                                                                                                                                                                     Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                      Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                Nagayama K.,
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                  GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005426; F:ATP binding; IEA.
GO; GO:0005429; F:electron transporter activity; IEA.
GO; GO:0005439; F:RNA binding; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0008236; F:serine-type peptidase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:transferase activity; IEA.
GO; GO:000508; P:proteclysis and peptidolysis; IEA.
GO; GO:0005198; P:transcription; IEA.
                                                                                                                                                                                                                                                                                  Nagayama K., Kurosaki M., Enomoto N., "Characteristics of hepatitis C viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
               P:electron transport; IEA.
P:proteolysis and peptidolysis; IEA.
P:transcription; IEA.
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Pred. No. 1.2e-124;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44C34677649CB8DD CRC64;
                                                                                                                                                                                                                                                                                    Miyasaka Y., Marumo F., genome associated with
                                                                                                                                                                                                                                                                                                                                                             no
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01-OCT-2000 (TrEMBLrel. 17
O1-OCT-2003 (TrEMBLrel. 2
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Matches 288
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Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_erv; 1.
Pfam; PF01539; HCV_NS2; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF01001; HCV_NS48; 1.
Pfam; PF01001; HCV_NS48; 1.
Pfam; PF01506; HCV_NS58; 1.
Pfam; PF01506; HCV_NS58; 1.
Pfam; PF01506; HCV_NS58; 1.
Pfam; PF01506; HCV_NS1; 1.
Pfam; PF01506; HCV_NS1; 1.
Pfam; PF0186062; HCV_NS1; 1.
Pfam; PF0186062; HCV_NS1; 1.
PNART; SN04887; DENDO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SMO0487; LEAGUE, 1.
PROSITE; PS00190; CYTOCHROME C; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural
Coat protein; Envelope protein; Glycoprotein; Nandirected RNA polymerase; Transferase; Transferase; Transferase; 326763 MW; 1A48EE4BE51440D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0019079; P:viral genome replication; GO:0019087; P:viral transformation; IEA
                                                                                                                                                                                                                                                                                                                                                                                          904 AGITKVPYFVRAHGLIRACMLVRKVAGGHYLQMAFMKLAALTGTYVYDHLTPLRDWAHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | IPR002522; HCV_capsid.
| IPR002521; HCV_core.
| IPR002531; HCV_env.
| IPR002531; HCV_NS1.
| IPR002531; HCV_NS2.
| IPR002545; HCV_NS4a.
| IPR001490; HCV_NS4b.
| IPR001686; HCV_RGEP.
| IPR001686; HCV_RGEP.
                                                                                        GAGSKALAGQXGPVTQMYTNVDQDLVGWQAPPGARSLTPCT
                                                                                                                                                                                                                                 RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                                                                                                    GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                                                                             LRDLAVAVEPVVFSDMETKI ITWGADTAACGDI ISGLPVSARRGREILLGPADSLEGQGW
RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET
                                 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                          RLLAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR004109; Peptidase C29, IPR007095; RNA pol DS PS. IPR007094; RNA pol PSVir
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IPR000345; CytC_heme_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.6%; Score 1534; DB 12;
94.7%; Pred. No. 1.4e-124;
tive 10; Mismatches 6;
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Last sequence update)
Last annotation update)

Created)

3010 AA

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HASSP, PZOLOGIA

GO; GO:0015021;
GO; GO:0019028; C:viral env...
GO; GO:0019031; C:viral env...
GO; GO:0005524; F:AIF binding; Lm...
GO; GO:0005524; F:AIF binding; Lm...
R GO; GO:0005248; F:AIF dependent helicase.
R GO; GO:0005489; F:electron transporter activity.
DR GO; GO:0005489; F:shydrolase activity; IEA.
DR GO; GO:0005787; F:hydrolase activity; IEA.
DR GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0003968; F:skran-directed RNA polymerase activity; IEA.
DR GO; GO:0006318; F:structural molecule activity; IEA.
DR GO; GO:0006519; F:transferase activity; IEA.
DR GO; GO:000618; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0019087; P:viral genome replication; IEA.
DR GO; GO:0019087; P:viral genome replication; IEA.
DR InterPro; IPR00303; Cys Ser trypsin.
InterPro; IPR00345; CytC heme_BS.
InterPro; IPR002521; HCV_corpsid.

"TR002521; HCV_corpsid."
"TV_NS1."
        SON SEER LE LA LONG CONTRANTANTE LA LONG CONTRANTAN
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Viruses, ssRNA positive-strand viruses,
Hepacivirus.
NCBI TaxID=11103;
pfam; pP01001; HCV_NS4b; 1.
pfam; pP01506; HCV_NS5a; 1.
pfam; pP00771; heliGase C; 1.
pfam; pP00998; Viral_RdRP; 1.
probom; pD186062; HCV_NS1; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein; ATP-binding; Coat protein; protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 326692 MW; 074098DB305AFIA9 CRC64;
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PIR; A61196; A61196. 
PIR; PQ0246; PQ0246. 
PIR; PS0329; PS0329. 
HSSP; P26663; 1JXP.
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN M AND GLYCOPROTEIN E. THE N
PROTEIN C AND MRNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                         pF01543; HCV_capsid;

pF01542; HCV_core; 1.

pF01539; HCV_env; 1.

pF01560; HCV_NS1; 1.

pF01538; HCV_NS2; 1.

pF02907; HCV_NS3; 1.

pF01006; HCV_NS4a; 1.
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Peptidase C29.
RNA pol DS PS.
RNA pol PSvir.
capsid; 1.
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HCV core.
HCV env.
HCV NS1.
HCV NS2.
HCV NS4a.
HCV NS4b.
HCV NS5a.
HCV Rdrp.
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Query Match

86.6%;

Score 1534;

DB 12;

Length 3010;

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TMRS
                                                                       RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                       GAGSKTLAGPKGPITOMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                         GAGSKTLAGPKGP I TQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVI PVR
                                                                                                                                                                               RLLAPITAYSQOTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                     RRGDGRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMET
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1207
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Search completed: May 6, 2004, 09:35:44
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Result
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Maximum DB seq length: 200000000
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Perfect score
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2: /cgm2_6/ptodata/2,
3: /cgm2_6/ptodata/2,
4: /cgm2_6/ptodata/2,
5: /cgm2_6/ptodata/2,
6: /cgm2_6/ptodata/2,
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
Listing first 45 summaries
    MKKKKLEHHHHHHTSAGITK.....
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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 US-09-539-601-6
US-09-539-601-21
US-09-539-601-27
US-09-539-601-27
US-09-539-601-27
US-09-263-933-2
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US-09-919-901-11
US-09-919-901-11
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RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET

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Sequence Patent No	No. 66	Applicat	ion US	/095	39601C		
APPLI	CANT: E	Bartenso	hlager, I Hepatiti		lf FW C Virus Cell Culture S	ystem	
CURRE	ENT APPI	ICATION	MBER MBER	08-3	S/09/539,601C		
EARLIER APPEARLIER FIL NUMBER OF S	ER APPLICATION OF SEQ	DATE	МВЕК 1999-	. 04-	99 15 178.4 GERMANY 03		
SEQ II	NO 6			١			
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APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 2201
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-539-601-15
18
                                                                                     ; SEQ ID NO 3;
LENGTH: 3010;
TYPE: PRT;
CRGANISM: Hepatitis C virus
US-09-539-601-3
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                                  Query Match
Best Local Similarity
Matches 288; Conserv
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Sequence 15, Application US/09539601C
                                                                                                                                               APPLICANT: Bartenschlager, Ralf FW
APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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Pred. No. 2e-143;
9; Mismatches
                                      Score 1531; DB 4;
Pred. No. 3.2e-143;
9; Mismatches 7;
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Best Local Similarity
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Patent No. 6630343
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94.7%;
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GENERAL INFORMATION:
APPLICANT: Bartenschlager, Ralf FW
APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Cu
FILE REFERENCE: all sequences
CURRENT FAPPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERM
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
SECTION 210
                                                                                                                                                                                                                                                                                                964 LRDLAVAVEPVVFSDMETKVITWGADTAACGDIILGLEVSARRGREIHLGPADSLEGQGW
                                                                                                                         GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 255
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                                          RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET 315
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Pred. No. 3.2e-143;
9; Mismatches 7;
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RESULT 5 US-09-539-601-27

Sequence 27, Applica Patent No. 6630343 GENERAL INFORMATION:

Application US/09539601C

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                                                                                                                                APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOI
TITLE OF INVENTION: OF INHIBITORS OF THE HEI
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6280940
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Best Local Similarity 94.7%;
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TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ. ID NOS: 51
  Query Match
                                                                          LENGTH: 1692
TYPE: PRT
                                                     ORGANISM: Artificial Sequence
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  86.3%;
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Pred. No. 3.2e-143; 17:
  Score 1528;
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  DB 3;
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Length 1692;
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PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1692
TYPE: PRT
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 286; Conserv
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Matches 286; Conserv
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APPLICANT: Patick, Amy K.
APPLICANT: NOTICE, Amy K.
ITILE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILLING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
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94.1%; Pred. No. 2.7e-143;
tive 12; Mismatches 6; Indels 0
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12; Mismatches 6;
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RESULT 9
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US-09-263-933-2
Sequence 2, Application US/09919901
Patent No. 6599738
GRNERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
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CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 2
LENGTH: 2307
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Best Local
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FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,90
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 2307
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                                                                                                                                                APPLICANT: PORTES, Karen B.
APPLICANT: PORTES, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Portick, Amy K.
APPLICANT: PORTES GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0155-0055A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
**TORTES**: 1603**
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Patent No. 6280940
GENERAL INFORMATION:
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Best Local Similarity
Matches 286; Conserv
Query Match 86.1%; Score 1525; DB 3; Best Local Similarity 93.8%; Pred. No. 5.4e-143; Matches 285; Conservative 13; Mismatches 6;
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                                                                                                                                          ENGTH: 1692
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94.1%;
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Pred. No. 4.3e-143;
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                                          Length 1692;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
ITILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1998-08-08
PRIOR FILING DATE: 1998-08-08
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 1692
TYPE: PRT
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Best Local Similarity
Matches 285; Conserv
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Patent No. 659973
                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: : -09-919-901-11
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ORGANISM: Artificial
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       RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
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                                       AGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVR
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Sequence 9. Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Camp K.
APPLICANT: Patick, ON THE PATICAL FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0105A
CIURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
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; ORGANISM: Artificial Sequence US-09-263-933-9
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US-09-263-933-9
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Best Local S
Matches 285
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SEQ ID NO 9
LENGTH: 2307
TYPE: PRT
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APPLICANT: Potts, Karen B.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
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285; Conserv
TMRS 578
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RESULT 14

US-09-539-601-33

US-09-539-601-33

Sequence 33, Application US/09539601C

Patent No. 6630343

GENERAL INFORMATION:
APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PATENTING DATE: 1999-04-03
SEQ ID NO 33
LENGTH: 3010
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-539-601-33
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PRIOR FILING DATE: 1999-02-08
PRIOR PELLING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 9
LENGTH: 2307
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Best Local Similarity
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                                                                                                                         86.1%;
                                                                                                            Score 1524; DB 4; Length 3010; pred. No. 1.6e-142; 9; Mismatches 8; Indels 0
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Patent No. 6280940

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
ITILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT APPLICATION NUMBER: 09129,611
EARLIER APPLICATION NUMBER: 09129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOUTWARE PATENTING DATE: 1998-08-05
NUMBER: DESCRIPTION OF SEQ ID NOS: 33
SOUTWARE PATENTIN Ver. 2.0
LENGTH: 1692
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OM protein -

protein search, using sw model

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Minimum
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1: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*

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10: /cgn2_6/ptcdata/1/pubpaa/US09E_PUBCOMB.pep:*

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12: /cgn2_6/ptcdata/1/pubpaa/US09E_PUBCOMB.pep:*

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   US-10-017-736-4
US-10-50-585-4
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CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PastSEQ for Windows Version 4:0
SEQ ID NO 4
LENGTH: 334
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Best Local Similarity
Matches 334; Conserv
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TITLE OF INVENTION: Purified Active HCV NS2/3
FILE REFERENCE: 13/082
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; LENGTH: 334
; TYPE: PRT
; ORGANISM: HCV
US-10-650-585-4
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CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
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Publication No. US20040077066A1
GENERAL INFORMATION:
                                                                                                           Sequence 2, Application US/10017736
Publication No. US20020192640A1
GENERAL INFORMATION:
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Best Local
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3
FILE REFERENCE: 13/08
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
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Pred. No. 8.2e-163;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR PPLICATION NUMBER: 60/256,031
PRIOR RILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 409
TYPE: PAT
ORGANISM: HCV
US-10-650-585-2
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; TYPE: PRT
; ORGANISM: HCV
US-10-017-736-2
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Best Local Similarity 100.0%; Pred. No. 6e-152;
Matches 315; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10650585 Publication No. US20040077066A1 GENERAL INFORMATION:
                                                                                                                                                                       Matches 315;
                                                                                                                                                                                     Query Match
Best Local Similarity
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136 RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH 195
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                                   LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW
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                                                                                                                                                                       93.7%; Score 1660; DB 16;
100.0%; Pred. No. 6e-152;
tive 0; Mismatches 0;
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; LENGTH: 303
; TYPE: PRT
; ORGANISM: HCV
US-10-017-736-10
                                                                                             RESULT 6
US-10-650-585-10
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Sequence 10, Application US/10650585
Publication No. U320040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
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Publication No. US20020192640A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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Best Local Similarity
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APPLICANT: Boehringer Ingelheim (Canada) Ltd.
FITTLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 11/082
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR PILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 341
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PRIOR APPLICATION NUMBER: 60/256,031; PRIOR FILING DATE: 2000-12-15; PRIOR FILING DATE: 2000-12-15; NUMBER OF SEQ ID NOS: 21
SOPTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 10; LENGTH: 303
                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: HCV
US-10-017-736-14
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; ORGANISM: HCV
US-10-650-585-10
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Best Local S
Matches 303
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Publication No. US20020192640A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 303; Conservative
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LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW 135
                                                             RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
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                                                                                                                                        89.7%; Score 1589; DB 13; ilarity 100.0%; Pred. No. 3.5e-145; Conservative 0; Mismatches 0;
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APPLICANT: Boehringer Ingelheim (Canada) Ltd.
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
FILE REFERENCE: 13/082
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-15
NUMBER OF SEQ ID NOS: 21
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 341
RESULT 9
US-10-017-736-13
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US-10-650-585-14
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US-10-650-585-14
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             Application US/10017736
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100.0%; Prr
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APPLICANT: Boehringer Ingelheim (Canada) Ltd.
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
FITTLE OF INVENTION: Purified Active HCV NS2/3 Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Professor of the Pro
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FILE REFERENCE: 13/082

CURRENT FILING DATE: 2003-08-28

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: US/10/017,736A

PRIOR APPLICATION NUMBER: 05/256,031

PRIOR FILING DATE: 2000-12-14

PRIOR FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 352

TYPE: PAT

ORGANISM: HCV

US-10-650-585-13
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US-10-650-585-13
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Publication No. US20040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
APPLICANT: Brandinger Ingelheim (Canada) Ltd.
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Best Local Similarity
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Best Local Similarity
Matches 303; Conserv
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                                                                      89.7%; Score 1589; DB 16; ilarity 100.0%; Pred. No. 3.7e-145; Conservative 0; Mismatches 0;
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; LENGTH: 380
; TYPE: PRT
; ORGANISM: HCV
US-10-017-736-12
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US-10-017-736-12
(S-quence 12, Application US/10017736
; Sequence 12, Application US/10017736
; Publication No. US20020192640A1
; GENERAL INFORMATION:
; APPLICANT: Boethringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
; FILE REFERENCE: 13/082
; CURRENT APPLICATION UNUMBER: US/10/017,736
; CURRENT FILING DATE: 2001-12-14
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PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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Best Local Similarity
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TMR 380
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Query Match Best Local Similarity

89.7%;

Pred. No. 4.3e-145;

Length 393;

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Sequence 11, Application US/10017736
; Publication No. US20020192640A1
; GENERAL INFORMATION:
   APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Purified Active HCV NS2/3 Profile Reference: 13/082
; CURRENT APPLICATION NUMBER: US/10/017,736
; CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
; NUMBER: OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; CRCANISM: HCV
US-10-017-736-11
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APPLICANT: Behringer Ingelheim (Canada) Ltd.
FIITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
FRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-15
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOSFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 380
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; ORGANISM: HCV
US-10-650-585-12
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Best Local Similarity
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100.0%; Pred. No. 4.1e-145;
tive 0; Mismatches 0;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
FITTE OF INVENTION: Purified Active HCV NS2/3 Pro
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR APPLICATION NUMBER: US/256,031
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR APPLICATION NUMBER: 00/256,031
PRIOR APPLICATION NUMBER: 00/256,031
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 15
CORGANISM: HCV
US-10-650-585-11
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                  RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIFVESMET 315
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CURRENT APPLICATION NUMBER: US/10/017,736
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/256,031
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 303
; TYPE: PRT
; ORGANISN: HCV
US-10-017-736-18
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US-10-017-736-18
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Publication No. US20020192640A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 302; Conserv
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                                                                                      TMR 318
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                                                                  TMR
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                   2004, 09:43:18
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Pred. No. 2.2e-144;
0; Mismatches 1;
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ALIGNMENTS

RESULT 1 ABG32183 ABG32183 ABG32183 AC ABG3 AC HCV; enzyme; protease; NS2/3 (904-1206); hepatitis C virus infection; chronic liver disease; olirhosis; end-stage liver disease; virucide; hepatotropic; antinflammatory; lauryldiethylamine oxide; LDNO; chaotropic agent; mutant; mutein. 05-NOV-2002 13-DEC-2001; 2001WO-CA001796. 20-JUN-2002. WO200248375-A2 Synthetic. Hepatitis C virus. HCV protease NS2/3 truncation mutant 904-1206 ABG32183; ABG32183 standard; (first entry) protein; 303 Ã

The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal residue amino acid 810 to 906, or having a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length NS2/3 protease. Also included are (1) a composition (C) comprising an isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a mutated sequence, where the protease is in a solution comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide

Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.

WPI; 2002-599511/64.

Thibeault

'n

Lamarre D,

Maurice R,

Pilote ŗ

Pause

15-DEC-2000; 2000US-0256031P.

(BOEH) BOEHRINGER INGELHEIM CANADA LTD.

Claim 39; Page 58-59; 67pp; English.

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RESULT 2
ABG32182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 CC protease, involving isolating the protease in the presence of a CC chaotropic agent, refolding the isolated protease by contacting it with a CC reducing gent, and LDAO in the presence of reduced concentration of the CC chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 CC protease, involving diluting refolded inactive NS2/3 protease in a medium CC containing an activation detergent to induce auto-cleavage of the NS2/3 CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3 CC protease; involving incubating the active NS2/3 protease and produce cleavage products or their fragments, and measuring the presence or CC absence of uncleaved NS2/3 protease, cleavage products or their fragments, and measuring the presence of cc and (6) screening a potential inhibitor of auto-cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of, or CC absence of the potential inhibitor, comparing the amount of uncleaved NS2/3 protease, cleavage products or their fragments. The protease is CC useful for detailed biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of NS2/3 protease which are useful as therapeutic agents against HCV content sequence represents the NS2/3 truncation mutant 904-1206 (numbered relative to the full length NS2/3 protean)
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                                                                                                  HCV; enzyme; protease; NS2/3 (810-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 303 AA;
                                                                                                                                                                                                                                                                                                          ABG32182 standard; protein; 334 AA
                                                                                   chaotropic
                                                                                                                                                                                                                             05-NOV-2002
                                                                                                                                                                                                                                                                      ABG32182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                                                                                     agent;
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                                                                                                                                                                                       NS2/3
                                                                                                                                                                                                                             (first
                                                                                   disease; cirrhosis; end-stage liver disease; viru
antiinflammatory; lauryldiethylamine oxide; LDAO;
ent; 4K-5H (904-1206)st-4K; mutant; mutein.
                                                                                                                                                                                       truncation
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                                                                                                                                                                                         4K-6H (904-1206) st-4K.
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Hepatitis C virus Synthetic.

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AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG

AGITKVÞYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTÞLQDWAHAG

Query Match Best Local S Matches 303

Similarity

100.0%; ilarity 100.0%; Conservative C

0;

Score 1589; DB 5; Pred. No. 5.8e-146; Mismatches 0;

Length

0

Gaps

60 75

hes 303;

Sequence

334 AA;

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The invention relates to an isolated polypeptide consisting of a full-
CC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred
CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal
CC residue amino acid 810 to 906, or having a minimal amino acid sequence
CC from residues 904 to 1206 of hepatitis C virus (ECV) 1b-40 full-length
CC NS2/3 protease, Also included are (1) a composition (C) comprising a sufficient concentration of lauryldethylamine oxide (LDAO)
CC to prevent auto-cleavage of the protease; is in a solution
CC comprising a sufficient concentration of lauryldethylamine oxide (LDAO)
CC to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide
CC appearing as NB32198; (3) producing (M1) a refolded, inactive HCV NS2/3
CC protease, involving isolating the protease in the presence of a
CC chaotropic agent, refolding the isolated produced concentration of the
CC containing an activation detergent to induce auto-cleavage of the NS2/3
CC protease, involving diluting refolded inactive NS2/3 protease in amedium
CC containing an activation detergent to induce auto-cleavage of the NS2/3
CC protease, involving inclusting the auto-cleavage activity of NS2/3
CC protease, involving inclusting the auto-cleavage activity of NS2/3
CC protease, involving inclusting the auto-cleavage activity of NS2/3
CC protease, involving inclusting the auto-cleavage activity of NS2/3
CC protease, involving apotential inhibitor, comparing the presence of, or
CC absence of uncleaved NS2/3 protease, containing an active NS2/3 protease and produce
CC cleavage products or their fragments, and measuring the presence of, or
CC second of the potential inhibitor, comparing the amount of uncleaved
CC NS2/3 protease, involving carrying out M3 in the presence of, or
CC second of the potential inhibitor, comparing the amount of uncleaved
CC NS2/3 protease involving carrying out M3 in the presence of, or
CC protease with the comparing the products or their fragments
CC protease with the compari
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
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DB; ABK90407.
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ABG32III 1
ID ABG3
XX ABG3
XX ABG3
XX ABG3
XX ABG3
XX ABG3
XX HCV;
XX HCV;
XX HCV;
XX HCV;
XX HCD;
XX HCV;
XX HCD;

The invention relates to an isolated polypeptide consisting of a full-
length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred
to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal
residue amino acid 810 to 906, or having a minimal amino acid sequence
from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length
NS2/3 protease. Also included are (1) a composition (C) comprising an
isolated HCV NS2/3 protease selected from full length NS2/3 protease, or
its truncation or a mutated sequence, where the protease is in a solution
comprising a sufficient concentration of lauryldiethylamine oxide (LDAo)
to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide
appearing as AGG32198; (3) producing (M1) a refolded, inactive HCV NS2/3
protease, involving isolating the isolated protease by contacting it with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel
useful
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV; enzyme; protease; NS2/3 (866-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thibeault D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-2001; 2001WO-CA001796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 41; Page 62-63; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide for screening inhibitors of non-structural proteases l as therapeutic agents against hepatitis C virus, comprises full non-structural protease, or its truncation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc reducing agent, and LDAO in the presence of reduced concentration of the cc chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 protease, involving diluting refolded inactive NS2/3 protease in a medium containing an activation detergent to induce auto-cleavage of the NS2/3 protease, involving incubating the active NS2/3 protease in a medium corrected produces of the NS2/3 protease produced by M2 for sufficient time to induce auto-cleavage activity of NS2/3 cc protease, involving incubating the active NS2/3 protease and produce corrected products or their fragments, and measuring the presence or cleavage products or their fragments, and measuring the presence of active NS2/3 protease, involving carrying out M3 in the presence of a cc absence of the potential inhibitor, comparing the amount of uncleaved cr absence of the potential inhibitor, comparing the amount of uncleaved cc useful for detailed biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of confection (which causes chronic liver disease, cirrhosis and end-stage cliver disease. M1 is useful for high level production of protease. The present sequence represents the NS2/3 truncation mutant 866-1206 (numbered relative to the full length NS2/3 protein)
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Best Local S
Matches 303
                                                                                                                             HCV; enzyme; protease; NS2/3 (855-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO;
                                                                                                                                                                                                                                  05-NOV-2002
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                                                                                                               chaotropic
                                                                                                                                                                                                                                                                   ABG32186;
                                                                                                                                                                                                 protease NS2/3 truncation
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                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                  TMR 341
                                                                                                                 agent;
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Pred. No. 6e-146;
0; Mismatches 0
                                                                                                                                                                                                 mutant 855-1206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
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Hepatitis C virus

WO200248375-A2

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The invention relates to an isolated polypeptide consisting of a full-college to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence college from residues 904 to 1206 of hepatitis C virus (HCV) 1D-40 full-length CC NS2/3 protease. Also included are (1) a composition (C) comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) CC comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) CC comprising as sufficient concentration of lauryldiethylamine oxide (LDAO) CC comprising as ABG32198; (3) prodease; (2) a NS2/3 inhibitory peptide concentration of lauryldiethylamine oxide (LDAO) CC chaotropic agent, and LDAO in the protease in the presence of a twith a C reducing agent or a polar additive; (4) producing (M1) an active NS2/3 CC protease, involving isolating the isolated protease by contacting it with a C reducing an activation detergent to induce auto-cleavage of the NS2/3 protease in a medium C containing an activation detergent to induce auto-cleavage of NS2/3 protease in a medium C containing an activation the auto-leavage activity of NS2/3 CC protease, involving incubating the active NS2/3 protease and produce c absence of uncleaved NS2/3 protease, involving incubating the active NS2/3 protease and produce c absence of uncleaved NS2/3 protease, cleavage products or their fragments, and measuring the presence or active NS2/3 protease, involving carrying out M3 in the presence of c absence of the potential inhibitor, comparing the amount of uncleaved CNS2/3 protease, cleavage products or their fragments of the presence of the development of in vitro assays for screening novel inhibitors of state activity of an activative of active NS2/3 protease in a medium c their fragments. The protease is contained to the full length NS2/3 truncation mutant 855-1206 c liver disease. M is useful for high level production of protease. The protease.
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                                                                                                                                                                                                                                                                                                                          Matches 303;
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 41; Page 61-62; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-599511/64.
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                                                                                                                                                  LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW
                                                                                                                                                                                                                                                                            AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
                                                           RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
                                                                                         RLLAPITAYSQQTRGLLGCIITSLIGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
                                                                                                                                                                                                                                     AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
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Pred. No. 6.3e-146;
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The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred CC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred CC slowers) as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence (NS2/3 protease) also included are (1) a composition (C) comprising an isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a mutated sequence, where the protease is in a solution (C) comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) (C) prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 (C) protease, involving isolating the protease in the presence of a (C) chaotropic agent, and LDAO in the presence of reduced concentration of the containing an activation detergent to induce auto-cleavage of the NS2/3 (C) protease, involving incubating the active NS2/3 protease in a medium (C) measuring (M3) the auto-cleavage activity of NS2/3 (C) protease, involving incubating the active NS2/3 protease and produce (C) measuring (M3) the auto-cleavage activity of NS2/3 (C) protease, involving the active NS2/3 protease and produce cleavage products or their fragments, and measuring the presence of containing a potential inhibitor of auto-cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of, or absence of the potential inhibitor, comparing the amount of uncleaved is sense of the potential inhibitor, comparing the amount of uncleaved is sense of the potential inhibitor, comparing the amount of uncleaved is sense in the presence of, or active NS2/3 protease, cleavage products or their fragments or their fragments. The protease is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptide for screening inhibitors of non-structural useful as therapeutic agents against hepatitis C virus, compr length non-structural protease, or its truncation.
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Best Local Simi
Matches 303;
                                                                                                                                                                                                                                                                                                                                          HCV; enzyme; protease; NS2/3 (815-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for detailed biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of NS2/3 protease which are useful as therapeutic agents against HCV infection (which causes chronic liver disease, cirrhosis and end-stage liver disease. MI is useful for high level production of protease. The present sequence represents the NS2/3 truncation mutant 827-1206 (numbered relative to the full length NS2/3 protein)
Novel polypeptide for useful as therapeutic
                                                                                                                                                                              13-DEC-2001; 2001WO-CA001796
                                                                                                                                                                                                               20-JUN-2002
                                                                                                                                                                                                                                                                                             Hepatitis C virus
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100.0%; Pred. No. 7e-146;
screening inhibitors of non-structural proteases agents against hepatitis C virus, comprises full
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                                                                               Maurice
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Claim 41; Page 59-60; 67pp; English

Collength HCV (hepatitis to an isolated polyperiode consisting of a rulfCC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred
CC residue amino acid 810 to 906, or having a minimal amino acid sequence
CC from residues 904 to 1206 of hepatitis C virus (HCV) 11-40 full-length
CC NS2/3 protease. Also included are (1) a composition (C) comprising an
CC isolated HCV NS2/3 protease selected from full length NS2/3 protease.
CC comprising a sufficient concentration of lawyldiethylamine oxide (LDAO)
CC or prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide
CC protease, involving isolating the isolated protease by contacting it with a
CC reducing agent, refolding the isolated protease by contacting it with a
CC reducing agent, and LDAO in the presence of reduced concentration of the
CC chaotropic agent or a polar additive; (4) producing (M1) an active NS2/3
CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3
CC protease; involving incubating the active NS2/3 protease in a medium
CC containing an activation detergent to induce auto-cleavage of the NS2/3
CC protease; involving incubating the active NS2/3 protease and produce
CC leavage products or their fragments, and measuring the presence or
CC absence of uncleaved NS2/3 protease, cleavage products or their fragments, and measuring the presence or
CC active NS2/3 protease, cleavage products or their fragments of uncleaved
CC NS2/3 protease, cleavage products or their fragments. The protease and in
CC useful for detailed biochemical characterisation of the enzymes and in
CC the development of in vitro assays for screening novel inhibitors of
CC useful for detailed biochemical characterisation of the enzymes and in
CC the development of in vitro assays for screening novel inhibitors of
CC useful for detailed biochemical characterisation of the enzymes and in
CC the development of in vitro assays for screening aspainst HCV
CC infection (which causes chronic liver disease, cirrhosis and end-stage
CC infection for the p invention relates to an isolated polypeptide consisting of 5th HCV (hepatitis C virus) non-structural (NS)2/3 protease a full-

Sequence 393 AA,

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Query Match
Best Local S
Matches 303
391
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                                                                            RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                   RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIFVESMET
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                                                                                                                                                   GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1589; DB 5; ilarity 100.0%; Pred. No. 7.3e-146; Conservative 0; Mismatches 0;
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RESULT ABG321 ID AI XX

81

ABG32181 standard; protein; 409

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The invention relates to an isolated polypeptide consisting of a full-color of the also as NS2/3 (810-1206)), or its truncation, having as its N-terminal cresidue amino acid 810 to 906, or having a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCW) lb-40 full-length CNS2/3 protease. Also included are (1) a composition (C) comprising as its notluded are (1) a composition (C) comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) CC to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide composition (S) comprising as protease, involving isolating the protease in the protease of a chaotropic agent, refolding the isolated protease by contacting it with a creducing agent or a polar additive, (4) producing (M1) an active NS2/3 containing an activation detergent to induce auto-cleavage of the NS2/3 protease in a medium containing an activation detergent to induce auto-cleavage of the NS2/3 containing an activation detergent to induce auto-cleavage of the NS2/3 protease; (5) measuring (M3) the auto-leavage activity of NS2/3 containing an activation detergent to induce auto-cleavage of the NS2/3 protease, involving incubating the active NS2/3 protease and produce cleavage products or their fragments, and measuring the presence of active NS2/3 protease, involving carrying out m3 in the presence of cleavage products or their fragments, and measuring the amount of uncleaved (NS2/3 protease, cleavage products or their fragments of the presence of or their fragments. The protease is involving carrying out m3 in the presence of, or active NS2/3 protease, involving carrying out m3 in the presence of, or active NS2/3 protease, involving carrying out m3 in the presence of, or active NS2/3 protease, oleavage products or their fragments. The protease is cleavage activity of an active NS2/3 protease of manual streptanion and safety active active active active active active active active active active active active active active active active active active active activ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thibeault D,
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Best Local
                              Novel polypeptide for useful as therapeutic length non-structural
                                                                                                                                                                                                                                                                  Hepatitis C virus.
Synthetic.
                                                                                                                                                                                                                                                                                                 HCV; enzyme; protease; NS2/3 (904-1206); hepatitis C virus infection; chronic liver disease; clirhosis; end-stage liver disease; virucide; hepatotropic; antinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 409 AA;
                                                                         WPI; 2002-599511/64.
                                                                                                                                                           13-DEC-2001; 2001WO-CA001796
                                                                                                                                                                                                                                ney Location/Qualifiers Misc-difference 90
                                                                                                                                                                                                                                                                                                                                                       HCV protease NS2/3 truncation 904-1206/Cys993Ala
                                                                                                                                                                                                                                                                                                                                                                            05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                ABG32191;
                                                                                                                                                                                                                                                                                                                                                                                                                    ABG32191 standard; protein; 303
          Disclosure; Page 65-66; 67pp; English.
                                                                                                                                                                                                      WO200248375-A2
                                                                                                                                       15-DEC-2000; 2000US-0256031P
                                                                                                                  (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
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                                                                                              Lamarre
                                                                                                                                                                                                                          /note= "Wild-type Cys substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                              screening inhibitors of non-structural agents against hepatitis C virus, compoundation.
                                                                                              'n
                                                                                              Maurice R,
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Pred. No. 7.8e-146;
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HCV protease NS2/3 truncation 904-1206/His952Ala.

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containing an activation of the protease in a medium general for protease, involving the protease is an activation of the protease, in a metative (M2/3) protease selected from the protease is an activation of the protease in a medium general for comprising an unitated sequence, where the protease is in a solution comprising as fift into protease, or comprising a sufficient concentration of lauryldisthylamine oxide (LDAO) or to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 comprising a protease, involving isolating the protease in the presence of a reducing agent, refolding the protease in the presence of a containing an activation detergent to induce auto-cleavage of the NS2/3 containing an activation detergent to induce auto-cleavage of the NS2/3 protease; (5) measuring (M3) the auto-cleavage of the NS2/3 protease; (5) measuring (M3) the auto-cleavage of the NS2/3 protease; (6) screening a potential inhibitor, and measuring the protease produced by M2 containing an activate NS2/3 protease; (5) measuring the auto-cleavage of NS2/3 protease and produce containing a potential inhibitor, comparing the presence of active NS2/3 protease, involving incubating the active NS2/3 protease and produce containing a potential inhibitor, comparing the amount of uncleaved NS2/3 protease, cleavage products or their fragments, and measuring the presence of, or cative NS2/3 protease, cleavage products or their fragments of auto-cleavage activity of an active NS2/3 protease, cleavage products or their fragments. The protease is credit for detailed biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of confection (which causes chronic liver disease, cirrhosis and end-stage in the development of invitro assays for screening novel inhibitors of confection (which causes chronic liver disease, cirrhosis and end-stage in the protease. The confection of the cause of the NS2/3 t
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to also as NS2/3 (gresidue amino acid
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GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                        GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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NS2/3 (810-1206))
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ilarity 99.7%;
Conservative
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Pred. No. 3.8e-145;
0; Mismatches 1;
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Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                      (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
                                                                                                                                                                                                                                                                                                                          2002-599511/64.
                                                                                                                                                                                                                                                                                                                                       Lamarre D,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild-type His substituted by
                                                                                                                                                                                                                                                                                                                                       Maurice R, Pilote
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                                                                                                                                                                                                                                                                                                                                       Pause
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Example 7; Fig 8; 67pp; English

The invention relates to an isolated polypeptide consisting of a full-clearly the CV (hepatitis C virus) non-structural (NS)2/3 protease (referred CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence CC from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC NS2/3 protease. Also included are (1) a composition (c) comprising a nutrated sequence, where the protease is in a solution comprising a sufficient concentration of lauryldiathylamine oxide (IDAO) CC to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide capearing as 88032198; (3) producing (M1) a refolded, inactive HCV NS2/3 protease, involving isolating the protease in the presence of a reducing agent, refolding the isolated protease by contacting it with a cc chaotropic agent, and LDAO in the presence of reduced concantration of the NS2/3 protease; (5) measuring (M2) an active NS2/3 protease; (5) measuring diluting refolded inactive NS2/3 protease, involving incubating the auto-cleavage activity of NS2/3 protease, involving incubating the auto-cleavage activity of NS2/3 protease, involving incubating the active NS2/3 protease produced by M2 capearing (M2) an active NS2/3 protease, involving incubating the active NS2/3 protease and produce cleavage produces or their fragments, and measuring the presence of containing a potential inhibitor of auto-cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of, or absence of the potential inhibitor, comparing the amount of uncleaved containing the potential inhibitor of auto-cleavage activity of an active NS2/3 protease is involving carrying out M3 in the presence of, or absence of the potential inhibitor of auto-cleavage activity of an active NS2/3 protease with a residual produce of active to a capear and active to a capear and active to a capear and active to a capear and active to a capear and active to a capear and active to a capear and acti

Sequence 303 8

RESULT 9
ABG32189
ID ABG3
XX
AC ABG3
XX
DT 05-N

ABG32189 standard;

protein;

303

05-NOV-2002

(first entry)

뮍 Ś 片 Ś В Ś 8 Ś Вb Š

RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET

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MR TMR 303

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Matches
  The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                      HCV; enzyme; protease; NS2/3 (904-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG32190 standard; protein; 301
                                                                            Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                WPI; 2002-599511/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCV protease
                                                     Example 7; Page 64-65; 67pp; English
                                                                                                                                                                                                            15-DEC-2000; 2000US-0256031P
                                                                                                                                                                                                                                      13-DEC-2001; 2001WO-CA001796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIFVESMET
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                                                                                                                                                            Lamarre
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                   "Wild-type Leu-Leu-Ala-Pro substituted by Leu-Pro"
                                                                                                                                                            Maurice R,
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cresidue amino acid 810 to 906, or having a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length CC MS2/3 protease. Also included are (1) a composition (C) comprising an CC isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a mutated sequence, where the protease is in a solution comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) to prevent auto-cleavage of the protease; (2), a NS2/3 inhibitory peptide appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 protease, involving isolating the protease in the presence of a CC chaotropic agent, refolding the isolated protease by contacting it with a CC chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 (CC protease, involving diluting refolded inactive NS2/3 protease; (5) measuring (M3) the auto-cleavage of the NS2/3 (CC protease, involving incubating the active NS2/3 protease produced by M2 protease, involving incubating the active NS2/3 protease and produce colleavage products or their fragments, and measuring the presence of a sheence of uncleaved NS2/3 protease, cleavage products or their fragments, and measuring the presence of colleavage products or their fragments, and measuring the amount of uncleaved NS2/3 protease, cleavage products or their fragments of the presence of or active NS2/3 protease, cleavage products or their fragments. The protease is cuseful for detailed biochemical characterisation of the enzymes and in cuter disease. Which causes chronic liver disease, cirrhosis and end-stage cliver disease. M1 is useful for high level production of protease. The colleavage produce tepresents the NS2/3 truncation 904-1206 mutant cc deltaled of autocatalytic activity
RESULT 11
ABG32188
ID ABG32
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XX
AC ABG32
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AC ABG32
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DT 05-NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 301 AA;
                                                          05-NOV-2002
                                                                                                                                ABG32188 standard; protein;
                   HCV protease NS2/3 truncation
                                                                                           ABG32188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGITKVDYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLJALIGTYVVDHLIPDLQDWAHAG
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                                                                                                                                                                                                                         TMR 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                          (first entry)
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Pred. No. 3.6e
0; Mismatches
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                       mutant 915-1206
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The invention relates to an isolated polypeptide consisting of a full-CC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal CC residue amino acid 810 to 906, or having a minimal amino acid sequence CC from residues 904 to 1206 of hepatitis C virus (HCV) lb-40 full-length CC (NS2/3) protease. Also included are (1) a composition (C) comprising an CC isolated HCV NS2/3 protease selected from full length NS2/3 protease, or CC comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) CC to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide CC appearing as ABG22198; (3) producing (M1) a refolded, inactive HCV NS2/3 protease, involving isolating the isolated protease by contacting it with a CC chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 cc protease, involving diluting refolded inactive CO contentration of the cc chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 protease; (5) measuring (M3) the auto-cleavage of the NS2/3 protease in a medium CC cleavage products or their fragments, and measuring the presence of a protease; (5) measuring (M3) the auto-cleavage of NS2/3 protease produced NS2/3 protease, involving incubating the active NS2/3 protease produced by M2 cc active NS2/3 protease, involving incubating the active NS2/3 protease produced or their fragments, and measuring the presence or absence of uncleavage products or their fragments or their fragments of cleavage activity of an active NS2/3 protease, involving carrying out M3 in the presence of, or absence of the potential inhibitor, comparing the amount of uncleaved consentual inhibitor, comparing the amount of uncleaved consents of the protease in a steril for their fragments. The protease is cleavage activity of an active NS2/3 protease is in a schilar for high level production of the enzymes and in the decrease in the interdiscent of the consents and end-stage consents agains
                                                                                    Query Match
Best Local S
Matches 292
                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length non-structural protease,
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide for screening inhibitors of non-structural as therapeutic agents against hepatitis C virus, compa
                     12 AQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPV
                                                                                                        Similarity
                                                                                                                                                                    292
AGGLIRACMLVEKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPV
                                                                                      Conservative
                                                                                                                                                                    ΑA;
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                                                                                                     96.4%;
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                                                                                    0,
                                                                                                 Score 1532; DB 5; I
Pred. No. 1.7e-140;
                                                                                    Mismatches
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                                                                                                                                                                                                                                                20-DEC-2001; 2001WO-CA001843
                                                                                                                                                                                                                                                                                 WO200252015-A2
                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                       Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C
                                                                                                                                                                                                               (BOEH ) BOEHRINGER INGELHEIM CANADA LTD
                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG30601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPITOMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QTRGLLGCTTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIFVRRRGDSRGSLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPK 191
                                                                                                                                                                                                                                                                                                                                                                                               virus NS2/3, NS3/4, NS3 and NS5B mutant #10
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
882
                                                                                                                                                                                                                                                                                                         2183
                                                                                                                                                                                                                                                                                              /note= "Wild type Met substituted by Thr"
                                                                                                                                                                                                                                                                                                                .abel= Arg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
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Claim 3; Page; 140pp; English. New self-replicating RNA molecules from Hepatitis C virus (HCV), wh possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.

Kukolj G,

Pause A;

2002-575382/61.

The invention describes a self-replicating hepatitis C virus (HCV)

C polynucleotide molecule comprising a 5'-non translated region (NTR),

Where guanine at position 1 is substituted for adenine, a HCV polyprotein

C region coding for a HCV polyprotein; and a 3'-NTR region. The self
C replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating

C potential inhibitors of HCV replication. The HCV RNA molecule is also

C useful for efficiently establishing cell culture replication. The self
C replicating polynucleotide molecule contains a 5'-NTR, where G at

C position 1 is substituted for A, and therefore provides an alternative to

C existing systems comprising a self-replicating HCV RNA molecule that, in

C conjunction with mutations in the HCV non-structural region, such as the

C (2042)C/R mutations, transduces and/or replicates with greater

C efficiency. This amino acid sequence represents a mutant of the hepatitis

C virus replicon APGKI2 and contains the viral protease NS2/3, procease

C complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note:

B

72

IFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQ 131

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RESULT 13
ABG30591
ID ABG30
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Best Local
New self-replicating RNA molecules from Hepatitis C virus (HCV), wh possess enhanced transduction or replication efficiency, useful for
                                                                                                                                                                                                                                         Misc-difference 882
/label= Arg, Lys
                                                                                                                                                                                                                                                                             rey
Misc-difference 751
                                             WPI; 2002-575382/61.
                                                                       Kukolj G,
                                                                                                                             22-DEC-2000; 2000US-0257857P
                                                                                                                                                         20-DEC-2001; 2001WO-CA001843.
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                                                                                                                                                                                                                                                                                                                                                                    Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence does not appear in the specification but has been created from the wild type sequence shown in ABG30580 using information given in the claims of the invention
                                                                                                  (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
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                                                                       Pause
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                                                                                                                                                                                                                                                                    note= "Wild type Ser substituted by Gly"
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Pred. No. 4.6e-139;
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RESULT 14
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Best Local Similarity
Location/Qualifiers
Misc-difference 882
                                                                               Synthetic.
                                                                                                                                        Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                                                                                                                                                                                                   Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant #9.
                                                                                                                                                                                                                                             21-OCT-2002
                                                                                                                                                                                                                                                                                    ABG30600;
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                                                                                                  Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                evaluating potential inhibitors of HCV replication
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Pred. No. 4.6e-139;
8; Mismatches 7;
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/label= Arg, Lys

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local (
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Matches 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New self-replicating RNA molecules from Hepatitis C virus (HCV), which possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
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Search completed: May 6, 2004, 09:30:44 Job time : 42.2434 secs	Дb	8	DЬ	Ş
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T36248
B44212
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genome polyprotein - hepatitis C virus (strain JT) N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructur protein NS4a; nonstructural protein NS4b; nonstructural protein NS5 C;Species: hepatitis C virus

F;116-191/Product: envelope protein M #status predicted <PPM>F;192-389/Product: major envelope protein E #status predicted <MSE>F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>F;390-729/Product: nonstructural protein NS2 #status predicted <NS2>F;730-1006/Product: hepacivini #status predicted <NS3>F;1007-1615/Product: hepacivini #status predicted <NS3>F;1230-1237/Region: nuclectide-binding motif A (P-loop)
F;1312-1317/Region: nuclectide-binding motif B F;1316-1319/Region: DEXH motif F;1316-1319/Region: DEXH motif F;1316-1319/Region: DEXH motif F;1316-1319/Region: DEXH motif F;1316-1319/Region: DEXH motif P;1316-32013/Product: nonstructural protein NS4a #status predicted <N4A>F;1863-2013/Product: nonstructural protein NS5 #status predicted <N4B>F;2014-3010/Product: nonstructural protein NS5 #status predicted <N85>F;2014-3010/Product: nonstructural protein NS5 #status predicted <N85>F;2014-3010/P Ś 밁 Ś 片 Ś 밁 Ş A;Note: sequence extracted from NCBI backbone (NCBIN:106206, NCBIP:106207)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein;
F;2-115/Product: capsid protein C #status predicted <CPC> A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-3010 <TAN>
A;Cross-references: GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1; PID:g221613
A;Experimental source: HCY-JT R;Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; Hijikata, Virus Res. 23, 39-53, 1992
A;Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: A;Reference number: A45573; MUID:92295714; PMID:1318627
A;Accession: A45573 Query Match Best Local S Matches 289 1024 181 121 964 904 AAITAMPYFVRAQGLIRACMLVRKVAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG 61 LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW 120 289; ۲ Similarity GAGSKTLAGPKGPITQMYINVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 240 RLAPITAYAQQTRGLLGCIVTSLTGRDXNQVEGEVQVV8TATQSFLATCVNGVCWTVFH RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH 180 AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG LRDLAVAVEPVVFSDMETKIITWGADTAACGDIILGLPVSARRGREILLGPADSIEGQGW 96.4%; ilarity 95.4%; Conservative Score 1532; DB 1; Pred. No. 7.3e-124; 6; Mismatches 8; Length 3010; Indels <u>,</u> Gaps 1023 963 60 serine

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A; Molecule type: genomic RNA
A; Residues; 2650-2707 < KA2>
A; Residues; 2650-2707 < KA2>
A; Residues; 2650-2707 < KA2>
A; Residues; 2650-2707 < KA2>
A; Residues; 2650-2707 < KA2>
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A; Residues; 2650-2707 < KA2>
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A; Residues; 2650-2707 < KA2>
A; Residues; 2650-2707 < KA2>
A; Residues; 2650-2707 < KA2>
A; Residues; 2650-2707 < KA2>
A; Residues; 1040-2807 < KA2>
F; 116-191/Product; capsid protein C #status predicted < CEC>
F; 116-191/Product; major envelope protein M #status predicted < CEP>
F; 390-729/Product; major envelope protein E #status predicted < CEP>
F; 390-729/Product; major envelope protein NS1 #status predicted < CEP>
F; 300-1006/Product; nonstructural protein NS2 #status predicted < CEP>
F; 1107-1615/Product; hepacivirin #status predicted < CEP>
F; 1316-1317/Region; nucleotide-binding motif B
F; 1316-1319/Region; DEXH motif
F; 1316-1319/Region; DEXH motif
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N;Contains: capsid protein C; envelope protein M; major envelope protein E;
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 19-Jan-2001
C;Accession. 130-33: prones
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A;Title: Japanese isolates of the non-A, non
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R;Kato, N.; Hjjikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S
Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
A;Title: Molecular cloning of the human hepatitis C virus genome
A;Reference number: A39253; MUID:91088550; PMID:2175903
A;Accession: A39253
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Accession: PS0086
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                                                                                                 GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                           RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                    RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                 RILAPITAYSOOTRGLIGCIITSITGRDKNOVDGEVOVLSTATOSFLATCVNGVCWTVYH
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larity 94.4%;
Conservative 1
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Pred. No. 2e-123;
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A; Maccessium: AYOFT A; MA
A; Residues: 1-3010 CCHE>
A; Cross-references: GB:M84754
A; C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstructural
C; Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructural
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F;116-191/Product: major envelope protein B #status predicted <MEE>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;390-729/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F;1230-1237/Region: nucleotide-binding motif A [P-loop)
F;1316-319/Region: nucleotide-binding motif A [P-loop)
F;1316-319/Region: DEXH motif - Binding motif A [P-loop)
F;1363-2013/Product: nonstructural protein NS4 #status predicted <N4A>
F;1616-1862/Product: nonstructural protein NS5 #status predicted <N4B>
F;1014-3010/Product: nonstructural protein NS5 #status predicted <N55>
F;106,209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207;
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A;Title: The Taiwanese hepatitis C virus genome: sequence determination A;Reference number: A40244, MUID:92230206; PMID:1314449
A;Accession: A40244
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC
protein NS4a; nonstructural protein NS4b; nonstructural protein N
C;Species: hepatitis C virus
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992
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                                                                                                                                                                                                                                                 RLLAPITAYAQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYH
                                                                                                                                                                                                                                                                                                                                                  <u>LRDLAVAVEPVVFSDMETKIITWGADTAACGDIILGLPVSARRGREILLGPADSLEGRGW</u>
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93.1%;
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Pred. No. 2.6e-122;
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genome polyprotein

hepatitis

C virus

(isolate

RESULT S18030

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A;Cross-references: RMBL:X61591

A;Note: this sequence is inconsistent with the nucleotide translation

A;Note: this sequence is inconsistent with the nucleotide translation

A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320

as Trp, and TTC for residue 771 as Ser

A;Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)

C;Superfamily; hepatitis C virus genome polyprotein

C;Reywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serii

F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M*status predicted <AEDN>
F;127-199/Product: major envelope protein B #status predicted <AES>
F;300-729/Product: nonstructural protein NS1 #status predicted <ASS>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)

F;1312-319/Region: nucleotide-binding motif A (P-loop)
F;1312-319/Region: nucleotide-binding motif B
F;1616-1862/Product: nonstructural protein NS4 #status predicted <AMA>
F;1616-1862/Product: nonstructural protein NS4 #status predicted <AMA>
F;1616-197-product: nonstructural protein NS4 #status predicted <AMA>
F;1616-1862/Product: nonstructural protein NS5 #status predicted <AMA>
F;1616-209/234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (Amanus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S. Arch. Virol. 128, 163-169, 1993
A;Title: Sequence analysis of putative structural regions of hepatitis C virus A;Reference number: A48332; MUID:93119270; PMID:8380322
A;Accession: S33570
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A;Variety: isolate JK1
C;Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 23
C;Accession: S18030; S3570; A48332; S18029
C;Accession: S18030; S3570; A48380; S18029
C;Accession: S18029
C;Accession: S18029
C;Accession: S18029
C;Accession: S18029
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A;Residues: 1-3010 <HON>
A;Residues: 1-3010 <HON>
A;Cross-references: EMBL:X61596; NID:g59478; PIDN:CAA43793.1;
A;Experimental source: isolate JK1 from an individual
A;Experimental source: Known an individual
A;Experimental source: Known an individual
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A; Residues: 1-547, 'T', 549-62
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A; Accession: S18030
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Best Local Sin
Matches 280;
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11863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
12014-3010/Product: nonstructural protein NS5 #status predicted <NS5-
1204-3010/Product: nonstructural protein NS5 #status predicted <NS5-
1196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate
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                                                                                                                              RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                                                                                                                GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                                                                                                                                                                                  RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
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Pred. No. 7e-120;
9; Mismatches 1
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RESULT

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RESULT
S40770
                                                                                      genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein
protein NS4a; nonstructural protein NS4b; nons
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2
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F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4B>
F;1014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;106,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,
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A;Residues: 1-30.0 «TAK»
A;Residues: 1-30.0 «TAK»
A;Residues: 1-30.0 «TAK»
A;Cross-references: EMBL:MS8335; NID:g329770; PIDN:AAA72945.1; PID:g329771
A;Cross-references: EMBL:MS8335; NID:g329770; PIDN:AAA72945.1; PID:g329771
C;Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase;
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase;
F;2-115/Product: capsid protein C #status predicted <CPC»
F;116-191/Product: major envelope protein M #status predicted <NES»
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1»
F;390-1006/Product: nonstructural protein NS2 #status predicted <NS2»
F;300-1006/Product: nonstructural protein NS2 #status predicted <NS2»
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J. Virol. 65, 1105-1113, 1991
A;Title: Structure and organization of the
A;Reference number: A38465; MUID:91140698;
A;Accession: A38465
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC
protein NS4a; nonstructural protein NS4b; nonstructural protein N
C;Species: hepatitis C virus
                       submitted to the EMBL
                                                R;Okamoto,
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Jan-2001
                                                                     C; Accession:
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                                                                                                                                                                                                                                                                                                                1206
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BL Data
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                                                                       #sequence_revision; PC1285
                       Library,
                         March
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                                                                                            #text_change 19-Jan-2001
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A;Experimental source: isolate HC-JI
C;Superfamily; hepatitits C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop;
F;2-115/Product: capsid protein C #status predicted <CPC>
F;2-116-191/Product: envelope protein M #status predicted <EPM>
F;116-191/Product: manjor envelope protein E #status predicted <MED>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;300-729/Product: nonstructural protein NS2 #status predicted <NS1>
F;730-106/Product: hepacivirin #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS2>
F;1312-331/Region: nucleotide-binding motif A (P-loop)
F;3312-331/Region: DEXH motif
A;Accession: A39166
A;Kolecula type: mRNA
A;Kolecula type: mRNA
A;Residues: 1-3011 <CHO>
A;Cross-references: GB:M62321; NID:g329873; PIDN:AAA45676.1;
A;Cross-references: GB:M62321; NID:g329873; PIDN:AAA45676.1;
A;Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer,
R;Chan, S.W.; McOmish, T.; Holmes, E.C.; Dow, B.; Peutherer,
R;Chan, Virol. 73, 1131-1141, 1992
                                                                                                                                            genome polyprotein - hepatitis C virus (strain HCV-1)
genome polyprotein - hepatitis C virus (strain HCV-1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 19-Jan-2001
C;Accession: A39166; PQ0403; FQ0404
R;Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegeroo.
Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A;Title: Genetic organization and diversity of the hepatitis C virus.
A;Reference number: A39166; MUID:91172826; PMID:1848704
A;Accession: A39166; MUID:91172826; PMID:1848704
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A;Cross references: EMBL:D10749; NID:g221586; PIDN:BAA01582.1; PID:g221587
R;CKamoto, H.; O'Adda, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa,
Tpn. J. Exp. Med. 60, 167-177, 1990
A;Title: The 5'-terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284; MUID:91013116; PMID:2170712
A;Reference number: PC1284; MUID:91013116; PMID:2170712
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A; Residues: 1-513 < OK2>
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;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
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HC-J1
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Pred. No. 1.1e-112;
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RESULT
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N;Contains: capsid protein C; envelope protein M; hepaciv
protein N84a; nonstructural protein N84b; nonstructural
C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_
C;Note: 33-Dec-1992 #sequence_revision 31-Dec-1992 #text_
A;Description: Genomic struc
A;Reference number: A36814
A;Accession: A36814
A;Molecule type: genomic RNA
A;Residues: 1-3011 <INC>
                                                                       C;Accession: A36814; A41546
R;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, submitted to GenBank, July 1992
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A;Experimental source: isolates
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A; Residues: 1577-1633
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Pred. No. 2.9e+112;
Pred. No. 2.3e+112;
                                                            prototype
                                                                                                                                                                                H)
M; hepacivirin (EC
                                                                                                                    #text_change 19-Jan-2001
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A;Cross-references: GB:M67463; NID:g329737; PIDN:AAA45534.1; PID:g329738
R;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A;Title: Genomic structure of the human protocype strain H of hepatitis C virus: compari A;Reference number: A41546; MUID:92052256; PMID:1658800
A;Contents: annotation
A;Note: neither amino acid nor nucleotide sequence is given
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; hydrolase; nonstructura
F;116-191/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: major envelope protein M #status predicted <CPC>
F;119-389/Product: nonstructural protein NS1 #status predicted <NS1>
F;300-729/Product: nonstructural protein NS2 #status predicted <NS1>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;3112-1317/Region: nucleotide-binding motif A (P-loop)
F;3116-1362/Product: nonstructural protein NS4 #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4 #status predicted <N55>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <N55>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
                                                                                                                                                                                                                                                                                                                                               genome polyprotein - hepatitis C virus (isolate EUH1480) N;Contains: capsid protein C; envelope protein M; hepacivirin (EC protein NS4a; nonstructural protein NS4b; nonstructural protein NG;Species: hepatitis C virus C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19 C;Accession: JC5620
A;Experimental source: genotype 5a, which predominates in South Africa A;Note: the translation of the nucleotide sequence is not complete in C;Superfamily: hepatitis C virus genome polyprotein C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; F;2-115/Product: capsid protein C #status predicted <CPC>
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                                                                                                                                     A; Residues: 1-3014 < CHA>
A; Cross-references: GB:Y13184
                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A;Title: The complete coding sequence of hepatitis C virus genotype
A;Reference number: JC5620; MUID:97366593; PMID:9223423
A;Accession: JC5620.
                                                                                                                                                                                                                                                                                                       R;Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, Biochem. Biophys. Res. Commun. 236, 44-49, 1997
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; Pred. No. 3.9e-111;
26; Mismatches 23;
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genome polyprotein - hepatitis C virus (isolate HC-J6)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nc
protein NS4a; nonstructural protein NS5b; nonstructural protein NS5
C;Spacies: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 17-Nov-2000
C;Accession: JQ1303
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H.; Machida, A.; Miya
J. Gen. Virol. 72, 2697-2704, 1991
A;Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated fr
A;Reference number: JQ1303
A;Accession: JQ1303
A;Accession: JQ1303
A;Accession: JQ1303
A;Accession: JQ1303
A;Accession: JQ1303
A;Accession: JQ1303
A;Cosa-references: GB:D00944; NID:9221650; PIDN:BAA00792.1; PID:9221651
A;Cross-references: GB:D00944; NID:9221650; PIDN:BAA00792.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kurai, K.; Iizuka, H.; Machida, A.; Miyakawa,
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F;196,209,234,305,325,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038, Length 3033;

Db. 밁 S В δ 맑 Ş 片 Ş S Query Match Best Local . Locar 209; 1150 1090 1030 183 123 243 970 910 63 ω Similarity LTRVPYFVRAHALLRMCTMVRHLAGGRYVOMVLLALGRWTGTYIYDHLTPMSDWAANGLR LAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGA GDKRGALLSPRPLSTLKGSSGGPVLCPRGHAVGVFRAAVCSRGVAKSIDFIPVETLDIVT GDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTM DLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGWRL LAPITAYAQQTRGLLGTIVVSMTGRDKTEQAGEIQVLSTVTQSFLGTTISGVLWTVYHGA DLAVAVEPIIFSPMEKKVIVWGAETAACGDILHGLPVSARLGREVLLGPADGYTSKGWSL 73.8%; Score 1172; DB 1; Pred. No. 1.1e-92; Mismatches 0

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122

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242 1089

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303

R 1210

RESULT 11

GNWV/B

genome polyprotein - hepatitis C virus (strain HC-J8)

yenome polyprotein C; envelope protein M; hepacivirin (EC 3.4.21.98)

N; Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)

protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C; Species: hepatitis C virus

C; Date: 31.Dec-1992 #sequence revision 31-Dec-1992 #text_change 19-Jan-2001

C; Accession: A40250; PQ0397; PQ0559

R; Okamoto, H.; Kurai, K.; Okada, S.I.; Yamamoto, K.; Lizuka, H.; Tanaka, T.

Virology 188, 331-341, 1992

A; Title: Full-length sequence of a hepatitis C virus genome having poor hom:
A; Reference number: A40250; MUID:92230232; PMID:1314459

A; Accession: A40250 3.4.21.98) NS5

T.; Fukuda, ťo

homology

repd

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A; Molecule type: genomic A; Residues: 1-3033 < OKA> genomic RNA

A;Cross-references: GB:D10988; GB:D01221; NID:9221608; PID R;Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peuthere J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its A;Reference number: PQ0393; MUID:92268871; PMID:1316939
A;Accession: PQ0397 GB:D01221; NID:g221608; PIDN:BAA01761.1; PID:g221609

phylogenetic relationship

A; Molecule type: genomic RNA
A; Residues: 2678-2754 < CIA>
A; Residues: 2678-2754 < CIA>
A; Cross-references: DDBJ:D10134
A; Experimental source: isolate E-b12
R; Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori
Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A; Title: Distribution of plural HCV types in Japan.
A; Reference number: PQ0554; MUID:92068204; PMID:1720309
A; Molecule type: mRNA
A; Residues: 2678-2729 < KAT>
A; Residues: 2678-2729 < KAT> s: Hijikata, 3 Shimotohno

hydrolase; nonstructur

A;Cross-references: GB:D10562; GB:D90518; NID:g221523; PIDN:BAA01418.1; PID:g221524
C;Superfamily: hepatitis C virus genome polyprotein
C;Seywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstruc
F;1-115/product: capsid protein C #status predicted <CPC>
F;116-191/product: envelope protein M #status predicted <AEPN>
F;192-389/product: major envelope protein NS1 #status predicted <AEPN>
F;390-733/product: nonstructural protein NS1 #status predicted <ASI>
F;734-1010/product: nonstructural protein NS1 #status predicted <ASI>
F;1011-1619/product: hepacivirin #status predicted <ASI>
F;1034-1241/Region: nucleotide-binding motif A (P-loop)

-000-000-1001-101

F;1316-1321/Region: nucleotide-binding motif B
F;1320-1322/Region: DEXH motif
F;1320-1322/Region: DEXH motif
F;1620-1866/Product: nonstructural protein NS4a #status predicted <N4A>
F;1867-2017/Product: nonstructural protein NS4b #status predicted <N4B>
F;2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
F;2018-3033/Produc

Query Match Best Local S Matches 204 204; Similarity Conservative 72.4%; 47; Score 1150; DB Pred. No. 9e-91; Mismatches DB 1; 52; Length 3033; Indels 0 Gaps

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멅 8 908 Н ASLLRIPYFVRAHALLRVCTLVKHLAGARYIQMLLITIGRWTGTYIYDHLSPLSTWAAQG AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG 967

Ś 片 Ś 121 896 61 RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH LRDLAIAVEPVVFSPMEKKVIVWGAETVACGDILHGLPVSARLGREVLLGPADGYTSKGW LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW 180 1027 120

å Ś 뮍 1028 181 GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR KLLAPITAYTOOTRGLLGAIVVSLTGRDKNEQAGQVQVLSSVTOTFLGTSISGVLWTVYH 240 1087

Ş 1088 241 RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET GAGNKTLAGPKGPVTQMYTSAEGDLVGWPSPPGTKSLDPCTCGAVDLYLVTRNADVIPVR 300

밁 1148 RKDDRRGALLSPRPLSTLKGSSGGPVLCSRGHAVGLFRAAVCARGVAKSIDFIFVESLDV 1207

Ś 1208 301 HMR 303

RESULT 12 T08841

(nonstruct)

#text_change 17-Nov-2000

polyprotein - douroucouli hepatitis GB virus A C;Species: douroucouli hepatitis GB virus A C;Ante: 20-Sep-1999 #sequence_revision 20-Sep-1999 C;Accession: T08841 F.Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, J. Gen. Virol. 79, 41-45, 1998 A;Ritle: Genomic analysis of two GB virus A variant: A;Reference number: Z16486; MUID:98120818; PMID:9468, A;Accession: T08841 A variants isolated; PMID:9460920 M.L.; Montes, from C.C.; Mushahwar, captive monkeys

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3005 <ERRN>
A;Cross-references: EMBL:AF023425; NID:g2828599; PIDN:AAC40502.1; PID:g2828600
C;Keywords: polyprotein

Query Match Best Local S Matches 95 l Similarity 95; Conser Conservative 25.0%; 46; Score 397.5; DB 2; Pred. No. 1.3e-25; 6; Mismatches 119; Length Indels 3005 13;

밁 8 34 AFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDI AFVRRLERRGVTLFQHCGQVSXGAAAILXDLGVALEPVSVTARDCYIVRDAARTLACGQR 946 93

Ş 94 ISGLPVSARRGREILLG--PADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQ 1005 151

Ś 片 947 HEGSIVVLGTSTTRSMGTCVNGVMYTTFHGSNARTLAGEVGEVNCRWWSESDDVAVYELP VEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGFKGPITQMYTNVDQDLVGWQAF VEGLEVVARRGDEVLVGVFPSVRALPPGFVPTAPVVV-MORGLGFFSVVKTSMLGRDERE

Ś 片 1006 PGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSG 271 1065

1066 SGASCLEPCKCGTQSVWCIRN--DGALCHGRLSKLVELDLPTEISDFRGSSGSPILCDEG

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C;Date: 23-Jul-1
C;Accession: T08
R;Erker, J.C.; D
J. Gen. Virol.
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B46642

C;Accession: B46642

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A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.
A;Reference number: Z16486; MUID:98120818; PMID:9460920
A;Accession: T08839
                                                                                                                                                                                                                                                       R;Miyazawa, H.; Izumi, M.; Tada, S.; Takada, R.; Masutani, M.; Ui, M.; Hanaoka, J. Biol. Chem. 268, 8111-8122, 1993
A;Title: Molecular cloning of the cDNAs for the four subunits of mouse DNA poly.
A;Reference number: A46642; MUID:93216788; PMID:8463324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-2970 <ERK>
                                                                                                                           A;Cross-references: GB:D13546; NID:g303658; PIDN:BAA02746.1; A;Experimental source: FM3A cells
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                                                                                                                                                                         A; Molecule type: mRNA; protein A; Residues: 1-600 < MIY>
                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                     A; Accession: B46642
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;Species: marmoset hepatitis GB virus A
;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 17-Nov-2000
;Accession: T08839
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                                                                                                         Note: sequence extracted from NCBI backbone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85;
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGHAVGML-ISVLHRGSRVTGIRYTKPWETLPREAITHT 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLIGVLNGV----WELPPGFVPTAPVVVH-HHGKGFFGVVKTSMTGWDETEHVGNVVVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILLGPADNFEGQGWRL-----LAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YAHAGQVTRRTAEQLRQWGFALEPVAVHPEDCAMVRDAARTLSCGQSVHGKPVVARRGDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                      6.4%;
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Pred. No. 1e-20;
16; Mismatches 96;
                      Score 101; DB 2; Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --RND--GALCHGTLGRTVELDLPAELCDFRGSSGSPILCD
  Mismatches
                                                                                                         (NCBIN:129148,
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  71;
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                                         Length 600
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                                                                                                                                                                                                                                                                                of mouse DNA polymerase
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  62;
Gaps
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LIRACMLVRKAAGGHYVQM-AFMKLAALT----

TPLQDWA

Search completed: May Job time: 10.8681 sec

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R,Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Drikin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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G87392
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C;Genetics:
A;Gene: CC1155
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Matches 72
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                                                                                                                                                                                                                                               ----GPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQS
                                                                                                                                                                                                                                                                                                                  TP-LODWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFL
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NFRSGQGAVLLTGGLAAGLMFLVANGMLTAL
                                                                                                                                                                         FLATCVNGVCWTVFHGAGSKTLAGPKGPIŢQMYTNVDQDĻVGWQAPPGARSMTPCTCGSS
                                                                                                                                                                                                               EKVEAPAARYDGKAWTLEQPKT---
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                                                                                                   DLYLVTRHADVIPVRRRGDSRGSLLSPRPVSY----LKGSSGGP-----LLCPSGHAVG
                                                                                                                                         -----ATSWP--
                                IFR----AAVCTRGVAKAVDFIPVESMETTM 302
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                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 99.5; DB 21.8%; Pred. No. 0.59; tive 36; Mismatches 1
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                                                                   --SDRPESFYATHLQAAFASPFVSLVMLLLSAPVALA
                                                                                                                                         ---TALRPQDVQGLFGDDSMPTAAS------
321
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Scoring table: Sequence: Title: Perfect score: OM protein -

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

Result

Score

% Query Match

398 1022 209 350 470 309 3491 453 TRMU AGRTS
CA26 CHICK
PAAD PSEAE
PE24 ARATH
NRAM IAUSS
HELS METAC
UCP2 HUVAN
PANE RHILO
ATCU YERPE
EXVI SACER
CRIB RHOCA
GAG_ĀVIMD Q987n5 Q8zca7 Q03131 P17056 P06444 Q8u9m5 P15988 Q9hx08 Q9zv04 P03469 Q8t139 P55851 agrobacteri gallus gall pseudomonas arabidopsis yersinia pe saccharopol rhodobacter influenza a methanosarc homo sapien rhizobium l

L Virus Res. 23:39-53(1992).

L Virus Res. 23:39-53(1992).

C -!- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are
C hydrophobic, suggesting a possible membrane-related function. NS3

C and NS5 may play a role in the viral RNA replication.

C encursor polyprotein, commonly with Asp or Glu in the viral
C precursor polyprotein, commonly with Asp or Glu in the P6

C position, Cys or Thr in P1 and Ser or Ala in P1'.

C -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +

C {RNA}(N).

C -!- SUBUNIT: The virion of this virus is a nucleocapsid covered by a

C lipoprotein envelope. The envelope consists of two proteins:
C procein M and glycoprotein E. The mucleocapsid is a complex of
protein C and mRNA.

C -!- SIMILARITY: THE PROTEASE BELCNGS TO PEPTIDASE FAMILY S29. DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-CT-2003 (Rel. 42, Last sequence update)
DT 01-CT-2003 (Rel. 42, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
DE Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
DE (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
DE (EC 3.4.21.9); Protease/helicase NS3 (P70) (Hepacivirin)
DE (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
DE NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
DE Viruses; SERNA positive-strand viruses, no DNA stage; Flaviviridae;
N NOBI TaxID=31642;
N (Il TaxID=31642; MEDLINE=92295714; PubMed=1318627;
Tanaka T., Kato N., Nakagawa M., Ootsuyama Y., Cho M.J.,
Nakazawa T., Hijikata M., Ishimura Y., Shimotohno K.;
Nakazawa T., Hijikata M., Ishimura Y., Shimotohno K.;
"Molecular cloning of hepatitis C virus genome from a single Japanese
carrier: sequence variation within the same individual and among
infected individuals.";

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Matches 289
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Pfam; PF01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J; IPRO02521; HCV_core.

J; IPRO02511; HCV_env.

J; IPRO02531; HCV_NS1.

J; IPRO02518; HCV_NS2.

J; IPRO02518; HCV_NS4.

J; IPRO01490; HCV_NS4.

J; IPRO01490; HCV_NS4.

J; IPRO01650; HelTcase_C.

J; IPRO01650; HelTcase_C.

J; IPRO07094; RNA_pol_DS_PS_PRO; IPRO07094; RNA_pol_DS_PS_PRO; IPRO07094; RNA_pol_DS_PS_PRO; IPRO07094; RNA_pol_DS_PS_PRO; IPRO07094; HCV_Core; 1.

J; IPRO1539; HCV_core; 1.

J; PPO1539; HCV_NS2; 1.

J; PPO1560; HCV_NS2; 1.

J; PPO1566; HCV_NS3; 1.

J; PPO1006; HCV_NS3; 1.

J; PPO1006; HCV_NS4; 1.

J; PPO1001; HCV_NS5; 1.

J; PPO1001; HCV_NS;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEMET
                                            al Similarity
289; Conserv
      AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALITGTYVYDHLTPLQDWAHAG
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2240
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3010
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nilarity 95.4%;
Conservative
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CAPSID PROTEIN ( POTENTIAL).

MATRIX PROTEIN ( POTENTIAL).

MAJOR ENVELOPE PROTEIN E ( POTENTIAL).

NONSTRUCTURAL PROTEIN NS1/E2 ( POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 ( POTENTIAL).

PROTEASE/HELICASE NS3 ( POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A ( POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B ( POTENTIAL).
                                            ; Score 1532; D
; Pred. No. 1.6e
6; Mismatches
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Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(BC 3.4.21.9); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein NS5B (P67); (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate Japanese) (HCV).
Viruses; SERNA positive-strand viruses, no DNA stage; Flaviviridae;
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01-AUG-1992 (Rel.
28-FEB-2003 (Rel.
                                                                                                                   MEDIINE=91088550; PubMed=2175903;
Kato N., Hijikata M., Ootsuyama Y., Nakagawa M., Ohkoshi Sugimura T., Shimotohno K.;
Sugimura T., Shimotohno K.;
"Molecular cloning of the human hepatitis C virus genome Japanese patients with non-A, non-B hepatitis.";
Proc. Natl. Acad. Sci. U.S.A. 87:9524-9528(1990).
                                                                                                                                                                                                                                             Kato N., Hijikata M., Nakagawa M., Ootsuyama Y.
Ohkoshi S., Shimotohno K.;
"Molecular structure of the Japanese hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P26662;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepacivirus.
                                                                                                                                                                                                                                                                                        MEDLINE=91192160;
                                                                                                                                                                                                                                                                                                      DISCUSSION OF SEQUENCE
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                                                 protein M and glycoprotein E. The nucleocapsid is a comprotein C and mRNA.
SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29
                                                                SUBUNIT: The virion of this virus lipoprotein envelope. The envelope protein M and glycoprotein E. The protein C and mRNA.
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M Nakagawa M.,
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                                                                       virus is a nucleocapsid covered envelope consists of two proteins. The nucleocapsid
                                                                                                                                                                                                                                                                               Ootsuyama Y.,
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W Polyprotein; Glycoprotein; Fransferase; RNA-directed RNA polymerase;
Core protein; Glycoprotein; Envelope protein; Helicase; ATP-binding;
W Transmembrane; Nonstructural protein; Hydrolase; Serine protease.
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InterPro; IPR001903; Cys Ser trypsin.

InterPro; IPR002522; HCV capsid.

InterPro; IPR002521; HCV core.

InterPro; IPR002521; HCV NS1.

InterPro; IPR002531; HCV NS2.

InterPro; IPR002531; HCV NS3.

InterPro; IPR002531; HCV NS4.

InterPro; IPR002531; HCV NS4.

InterPro; IPR002166; HCV NS4.

InterPro; IPR001499; Hellase C29.

InterPro; IPR001650; Hellase C29.

InterPro; IPR007094; RNA pol DS PS.

InterPro; IPR007094; RNA pol DS PS.

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InterPro; IPR007095; NNA pol DS PS.

InterPro; IPR007094; RNA pol DS PS.

InterPro; IPR007094; RNA pol DS PS.

InterPro; IPR007094; HCV NS3; 1.

Pfam; PF01543; HCV NS3; 1.

Pfam; PF01538; HCV NS3; 1.

Pfam; PF01506; HCV NS4a; 1.

Pfam; PF01006; HCV NS4a; 1.

Pfam; PF01006; HCV NS4a; 1.

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EQUENCE FROM N.A.

WINDLINE=92330206; PubMed=1314449;

WINDLINE=92330206; PubMed=1314449;

WINDLINE=92330206; PubMed=1314449;

WITH Taiwanese hepatitis C virus genome: sequence determination from mapping the 5' termini of viral genomic and antigenomic RNA.";

WINDLOYD 188:102-113(1992)

C -!- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function and NS5 may play a role in the viral RNA replication.

C -!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the precursor polyprotein, commonly with Asp or Glu in the P6 precursor polyprotein, commonly with Asp or Glu in the P6 precursor polyprotein, commonly with Asp or Glu in the P6 precursor polyprotein, commonly with Asp or Glu in the P6 precursor polyprotein, commonly with Asp or Glu in the P6 precursor polyprotein, commonly with Asp or Glu in the P6 precursor polyprotein of this virus is a nucleocapsid covered (RNA)(N).

C -!- SUBUNIT: The virion of this virus is a nucleocapsid covered lipoprotein M and glycoprotein E. The nucleocapsid is a complex protein M and glycoprotein E. The nucleocapsid is a complex protein C and mana. P29946;

D1-APR-1993 (Rel. 25, Created)

O1-APR-1993 (Rel. 25, Last sequence update)

O1-OCT-2003 (Rel. 42, Last annotation update)

10-OCT-2003 (Rel. 42, Last annotation update)

Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);

Envelope glycoprotein E1 (GP2) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)

(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)

(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS48 (P27); Nonstructural protein NS48 (P3); Nonstructural protein NS48 (P3); Nonstructural protein NS48 (P3); Nonstructural protein NS48 (P3); Nonstructural protein NS58 (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].

NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48);

Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; NCBI_TaxID=31645; HCVIW STANDARD; 3010 is a nucleocapsid covered e consists of two proteins nucleocapsid is a complex Lin C.J., Chen D.S.;
sequence determination
and antigenomic RNA."; diphosphate proteins: function. n the are γď Ģ, and

NS3

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DR InterPro; IPR009003; Cys Ser_trypsin.

DR InterPro; IPR001410; DEAD.

DR InterPro; IPR002521; HCV_capsid.

DR InterPro; IPR002525; HCV_capsid.

DR InterPro; IPR002531; HCV_core.

InterPro; IPR002531; HCV_core.

InterPro; IPR002531; HCV_NS1.

DR InterPro; IPR002531; HCV_NS4.

DR InterPro; IPR002531; HCV_NS4.

DR InterPro; IPR001499; HCV_NS4.

DR InterPro; IPR001550; HcV_NS4.

DR InterPro; IPR001650; HcV_NS4.

DR InterPro; IPR0017094; RNA_pol_pS_PS.

DR Ffam; PP01534; HCV_core; 1.

DR Pfam; PP01534; HCV_NS1; 1.

DR Pfam; PP01538; HCV_NS4; 1.

DR Pfam; PP01538; HCV_NS4; 1.

DR Pfam; PP01001; HCV_NS4; 1.

DR Pfam; PP01006; HCV_NS4; 1.

DR Pfam; PP0106; HCV_NS4;
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DIR; A40244; GNWVTW _

PDB; 1N64; 25-FEB-03.

PDB; 1N53; 08-APR-98.
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PROTEANS/HELICASE NG3 (POTENTIAL).
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MEDLLINE=96235224; PubMed=8647104;
Borowski P., Heiland M., Oehlmann K., Becker "Non-structural protein 3 of hepatitis C viru
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InterPro; IPRO09003; Cys Ser_trypsin.
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InterPro; IPRO002518; HCV_NS4a.
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InterPro; IPRO001490; HCV_NS4a.
InterPro; IPRO002868; HCV_NS5a.
InterPro; IPRO02166; HCV_NS4a.
InterPro; IPRO02166; HCV_RdRP.
InterPro; IPRO07095; RNA_pol_DS_PS.
InterPro; IPRO07095; RNA_pol_DS_PS.
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Love R.A., Parge H.E., Wickersham J.A., Hostomsky Z., Habuka N.,
Moomaw E.W., Adachi T., Hostomska Z.;
"The crystal structure of hepatitis C virus NS3 proteinase reveals a
trypsin-like fold and a structural zinc binding site.";
Cell 87:331-342(1996).
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SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF001508; Viral RdRp; 1.
ProDom; PD186062; HCV_NS1; 1.
SMART; SM00487; DEXDC; 1.
Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
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     CELLULAR AMMODEPTIDASE.

CAPSID PROTEIN C (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

MAJOR ENVELOPE PROTEIN NS1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).

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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Genome polyprotein E1 (G932) (G935); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.21.9); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS54 (P4); Nonstructural protein NS48 (P27); Nonstructural protein NS54 (P56); Nonstructural protein NS54 (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.3.48)).
Hepatitis C virus (isolate 1) (HCV).
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MEDLINE=1173826; PubMed=1848704;

Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C., Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J., Bradley D.W., Kuo G., Houghton M.;

"Genetic organization and diversity of the hepatitis C virus.";

"Genetic organization and diversity of the hepatitis C virus.";

Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455 (1991).

Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455 (1991).

-i- PUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function and NS5 may play a role in the viral RNA replication.

-i- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the catalytic active the process of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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                          precursor polyprotein, commonly with Asp or Glu in the position, Cys or Thr in pl and Ser or Ala in pl'. CAMALYTIC ACTIVITY: N nucleoside triphosphate = N dipho RNA) (N).
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InterPro; IPRO00745; HCV_NS4.
InterPro; IPRO00745; HCV_NS4.
InterPro; IPRO01409; HCV_NS5a.
InterPro; IPRO01650; Hclicase C.
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InterPro; IPRO01095; RNA_pol_DS_PS.
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InterPro; IPRO07094; RNA_pol_DS_PS.
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InterPro; IPRO07094; RNA_pol_PSVir.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_NS1; 1.
Pfam; PF01538; HCV_NS1; 1.
Pfam; PF01538; HCV_NS1; 1.
Pfam; PF01506; HCV_NS4a; 1.
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between the Swiss Institute of Bio.
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MAJOR SUVELOPE PROTEIN E (POTENTIAL).

MAJOR SUVELOPE PROTEIN MS1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
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01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein El (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein P7, Nonstructural protein NS2 (P21)
(EC 3.4.99.-); Protease/helicase NS3 (P70) (Hepactvirin)
(EC 3.4.21.98); Nonstructural protein NS46 (P4); Nonstructural protein
NS48 (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
                                              SEQUENCE FROM N.A.
MEDLINE=92052256; PubMed=1658800;
Inchauspe G., Zebedee S., Lee D.H.H.,
Prince A.M.;
"Genomic structure of the human prototoring structure of the human districtions with American and Japanese Proc. Natl. Acad. Sci. U.S.A. 88:10299
                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand
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U.S.A. 88:10292-10296(1991)
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Pred. No. 7e-113;
4; Mismatches 23;
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      C:- FUNCTION: PROTEASE NS2 IS RESPONSIBLE FOR THE CLEAVAGE OF NS2-NS3.

C:- FUNCTION: PROTEASE NS3 IS RESPONSIBLE FOR THE CLEAVAGE OF NS2-NS3.

C:- FUNCTION: NS4A FOLKS, NS4B-NS5A AND NS5A-NS5B.

C:- FUNCTION: NS4A FOLKS A COMPLEX WITH NS3 AND IS ESSENTIAL FOR THE CURVATION OF NS3.

C:- FUNCTION: NS5A SEEMS TO HAVE A TRANSCRIPTIONAL ACTIVATORY ROLE.

C:- FUNCTION: NS5B IS A RNA-DEPENDENT RNA POLYMERASE THAT PLAYS AN SEEMSTAL ROLE IN THE VIRUS REPLICATION.

C:- FUNCTION: NS5B IS A RNA-DEPENDENT RNA POLYMERASE THAT PLAYS AN ESSENTIAL ROLE IN THE VIRUS REPLICATION.

C:- FUNCTION: NS5B IS A NUA-DEPENDENT RNA POLYMERASE THAT PLAYS AN ESSENTIAL ROLE IN THE VIRUS REPLICATION.

C:- FUNCTION: NS5B IS A RNA-DEPENDENT RNA POLYMERASE IN THE PLAYS AN ESSENTIAL ROLE IN THE VIRUS SEPONDED E N A DEPENDENT RNA PLAYS AN ESSENTIAL ROLE IN THE VIRUS OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: E1

C:- FYN: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: E1

C:- FYN: THE NUCLEOCAPSID IS A COMPLEX OF PROTEINS: E1

C:- FYN: THE NS2 PROTEASE BELONGS TO PEPTIDASE FAMILY U39.

C:- SIMILARITY: THE NS2 PROTEASE BELONGS TO PEPTIDASE FAMILY U39.
                                                                                                                                                                InterPro; IPR00903; Cys Ser tryps
InterPro; IPR001410; DEAD.
InterPro; IPR001522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_env.
InterPro; IPR002519; HCV_NS1.
InterPro; IPR002518; HCV_NS4a.
InterPro; IPR000745; HCV_NS4a.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR00166; HCV_NS4b.
InterPro; IPR00166; HCV_RdRP.
InterPro; IPR002166; HCV_RdRP.
InterPro; IPR00160; Helicase_C.
InterPro; IPR00160; Helicase_C.
InterPro; IPR00160; Helicase_C.
InterPro; IPR00160; Helicase_C.
InterPro; IPR00160; Peptidase_C.
InterPro; IPR00160; Peptidase_C.
InterPro; IPR0017094; RNA_pol_DS_PS_INTERPRO; IPR007094; RNA_pol_DS_INTERPRO; IPR007094; RNA_pol_DS_PS_INTERPRO; IPR007094; RNA_pol_DS_PS_INTERPRO; IPR007094; RNA_pol_DS_PS_INTERPRO; IPR007094; RNA_pol_DS_PS_INTERPRO; IPR007094; RNA_pol_DS_PS_INTERPRO; IPR007094; RNA_pol_DS_PS_INTERPRO; IPR007095; RNA_pol_DS_PS_INTERPRO; IPR007095; RNA_pol_DS_PS_INTERPRO; IPR007095; RNA_PS_INTERPRO; IPR00
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PDB; 1HEI; 25-NOV-98.
PDB; 1A1V; 16-FEB-99.
PDB; 1A1R; 17-JUN-98.
MEROPS; S29.001; -.
    Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRANSFAC;
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MEDLINE=98154321; PubMed=9493270;
(007094; RNA_DOL_

HCV capsid; 1.

HCV core; 1.

HCV env; 1.

HCV_NS1; 1.

HCV_NS2; 1.

HCV_NS4a; 1.

HCV_NS4a; 1.
                                                                                                                                                                           Helicase C.
Peptidase C29.
RNA_pol_DS_PS.
PNNA_pol_DS_PS.
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WA helicase domain.
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pfam; PF00271; helicase C; 1.
pfam; PF00271; helicase C; 1.
pfam; PF00998; Viral_RdRP; 1.
proDom; PD18062; HCV_NS1; 1.
smART; SM00487; DEXDC; 1.
polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Polyprotein; Glycoprotein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
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PROTEASE/HELICASE NS3.
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS5A.
NONSTRUCTURAL PROTEIN NS5A.
NONSTRUCTURAL PROTEIN NS5B.
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PROTEIN P7.
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CAPSID PROTEIN C.
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RESULT 7

POLG HCVJ6 STANDARD; PRT; 3033 AA.

ID POLG HCVJ6 STANDARD; PRT; 3033 AA.

ID POLG HCVJ6 STANDARD; PRT; 3033 AA.

P26660;

O1-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Genome polyprotein [Contains; Capsid protein C (Core protein E2 Envelope glycoprotein E1 (GP22) (GP35); Envelope glycoprotein E2

DE Envelope glycoprotein E1 (GP22) (GP35); Envelope glycoprotein E2

DE (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)

DE (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS5A (P56); Nonstructural protein NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].

OS Hepatitis C virus (isolate HC-J6) (HCV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Pred. No. 9.4e
26; Mismatches
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Hepacivirus.
NCBI_TaxID=11113;
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WEDLINE=92044440; PubMed=1658196;
A Okamoto H., Okada S.-I., Sugiyama Y., Kurai K., Lizuka H.,
A Okamoto H., Okada S.-I., Sugiyama Y.,
A Machida A., Miyakawa Y., Mayumi M.;
A Machida A., Miyakawa Y., Mayumi M.;
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                                                                                                                                  InterPro; IPR009003, Cys Ser trypsin.
InterPro; IPR009003, Cys Ser trypsin.
InterPro; IPR002521; HCV_capsid.
InterPro; IPR002521; HCV_capsid.
InterPro; IPR002521; HCV_capsid.
InterPro; IPR002531; HCV_NS4.
InterPro; IPR002518; HCV_NS4.
InterPro; IPR0002518; HCV_NS4.
InterPro; IPR0002166; HCV_NS4.
InterPro; IPR00140; HCV_RdRP.
InterPro; IPR00150; Helicase_C2.
InterPro; IPR00150; Helicase_C2.
InterPro; IPR001094; RNA_Dol_DS_PS.
InterPro; IPR007095; RNA_Dol_DS_PS.
InterPro; IPR007094; RNA_Dol_DS_PS.
InterPro; IPR007094; RNA_Dol_PSvir.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_NS3; 1.
Pfam; PF01539; HCV_NS3; 1.
Pfam; PF01506; HCV_NS3; 1.
Pfam; PF01001; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS5a; 1.
Pfam; PF01006; HCV_NS5a; 1.
Pfam; PF010071; helicase_C.
Pfam; PF01071; helicase_C.
Pfam; PF01071; helicase_C.
Pfam; PF01071; DEXDC; 1.
SMARI; SN00487; DEXDC; 1.
SMARI; SN00487; DEXDC; 1.
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                                                            Polyprotein; Glycoprotein; Transferase; RNA-directed RNA Core protein; Coat protein; Envelope protein; Helicase; A Transmembrane; Nonstructural protein; Hydrolase; Serine p REMOVED FROM CAPSID PROTEIN
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        116
        CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C (POTENTIAL)
MATRIX PROTEIN (POTENTIAL).
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Matches 209
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P26661;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seq
28-FEB-2003 (Rel. 41, Last ann
Genome polyprotein [Contains: 0
Envelope glycoprotein E1 (GP3)
(GP68) (GP70) (NS1); Protein P
(EC 3.4.22.-); Protease/helica
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  el. 23, Last sequence update)
el. 41, Last annotation update)
tein [Contains: Capsid protein C (Core protein)
protein El (GP32) (GP35); Envelope glycoprotein
(NS1); Protein P7; Nonstructural protein NS2 (P2
Protease/helicase NS3 (P70) (Hapacivirin)
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GDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTM
                                                                                                                         LAPITAYAQQTRGLIGTIVVSMTGRDKTEQAGEIQVLSTVTQSFLGTTISGVLWTVYHGA
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Pred. No. 3e-93;
4; Mismatches
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NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL)
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NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE/HELICASE NS3 (POTENTIAL).
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InterPro; IPR009003; Cys Ser_trypsin.

RINTerPro; IPR002522; HCV_capsid.

RINTerPro; IPR002522; HCV_capsid.

RINTerPro; IPR002521; HCV_core.

RINTerPro; IPR002521; HCV_core.

RINTerPro; IPR002513; HCV_NS1.

RINTerPro; IPR002513; HCV_NS4.

RINTerPro; IPR002514; HCV_NS4.

RINTerPro; IPR002515; HCV_NS4.

RINTerPro; IPR002166; HCV_NS4.

RINTERPro; IPR002166; HCV_NS4.

RINTERPro; IPR002166; HCV_NS4.

RINTERPro; IPR002166; HCV_NS4.

RINTERPro; IPR001019; PEPTidase C29.

RINTERPRO; IPR001019; PEPTIDASE C30.

RINTERPRO; IPR00101
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SEQUENCE FROM N.A.

MEDLINE=92230232; PubMed=1314459;

MEDLINE=92230232; PubMed=1314459;

Okamoto H., Kurai K., Okada S.-I., Yamamoto K., Lizuka H., Tanaka Pukmda S., Tsuda F., Mishiro S.;

Pukmda S., Tsuda F., Mishiro S.;

"Full-length sequence of a hepatitis C virus genome having poor

"Full-length sequence of a hepatitis C virus genome having poor

"Full-length sequence of solates: comparative study of four distinct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
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NCBI_TaxID=11115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D10988; BAA01761.1;
PIR; A40250; GNWVJ8.
HSSP; P27958; 1HEI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Son send an email to license@isb-sib.ch).
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MEROPS; U39.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {RNA}(N).
SUBUNIT: The virion of this virus is a nucleocapsid covered lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex protein C and mRNA.
SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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RESULT 9
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PROTEASE/HELICASE NS3 (POTENTIAL).
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InterPro; IFR007200; DNA pol_alpha_B.
Pfam; PF040508; DNA pol_alpha_B; 1.
DNA replication; Nuclear protein; Phosphorylation.
DNA replication; Nuclear protein; Phosphorylation.
DOMAIN 101 107 POLY-GLU:
DOMAIN 101 157 PRO/SER/THR-RICH (HYDROPHILIC)
SEQUENCE 600 AA; 66267 MW; 79F94BE6EF33FEBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase alpha-primase complex and their cell proliferation and the cell cycle.";
J. Biol. Chem. 268:8111-8122(1993).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of the cDNAs for the four subunits of
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SUBUNIT: DNA
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etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Hepatitis E virus (strain Burma) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=31767;
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SIGNAL
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Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular cloning and sequencing of the
full-length viral genome.";
Virology 185:120-131(1991).
-i- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
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01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
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DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Structural protein 2 precursor (ORF2).

S Hepatitis E virus (strain Pakistan) (HEV).

C Viruses, ssRNA positive-strand viruses, no DNA st.

C Hepatitis E-like viruses.

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Malik I.A., Iqbal M., Purcell R.H.;
Micharacterization of a prototype strain of hepatitis E virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTINGENOMIC THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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RESULT 12 TRFE_HORSE

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EMBL; U21127; AAA63684.1; -.
PIR; S33761; S33761.
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                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUS SPECIFICITY: Expressed by the liver and
-!- DOMAIN: Composed of two homologous domains.
-!- SIMILARITY: Belongs to the transferrin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=93277958; PubMed=8504171;
Carpenter M.A., Broad T.E.;
"The CDNA sequence of horse transferrin.";
Biochim. Biophys. Acta 1173:230-232(1993).
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Mammalia; Eutheria; Perissodactyla;
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Eukaryota; Metazoa; Chordata;
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PROSITE; PS00206;
PROSITE; PS00207;
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SMART; SM00094; TR
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Pfam; PF00405; transferrin;
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TRANSFERRIN 3; 2.
ransport; Glycoprotein; Metal-binding;
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42, Last annotation
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MEDILINE=93079857; PubMed=1448913;
Huang C.C., Nguyen D., Fernandez,
Bradley D.W., Tam A.W., Reyes G.R.
"Molecular cloning and sequencing
E virus (HEV).";
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                  [1] T
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Ol-JAN-1990 (Rel. 13, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAY-2004 (Rel. 39, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Genome polyprotein [Contains: Capsid protein (Core protein); Matrix protein (Envelope protein M); Major envelope protein E; Nonstructural proteins NS1, NS2B, NS2B, NS4A and NS4B; Protease/helicase
(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC 2.7.7.48)
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SIGNAL
                                                                                                       Tick-borne encephalitis virus Viruses; ssRNA positive-strand Flavivirus.
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                                                                        NCBI_TaxID=11088;
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FROM N.A.,

AND

REVISIONS

(Western subtype)

(TBEV) stage;

Flaviviridae;

STANDARD;

PRT;

3414 AA

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Query Match
Best Local S
Matches 67
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B44212; B44212.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          send an email to license@isb-sib.ch).
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67; Conserv
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VATGAÇAVARSLDWSKV
                              AAVCTRGVAKAVDFIPV
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                                                                                                                        SSAGGQLFYSRPVVSANGEPTVKLYTSVENA----QQDKGVAIPHDIDLGDSRVVIQDYD
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                                                              NQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYI--SDSVTLVN
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659 AA;
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659 S
70640 MW;
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Pred. No. 4.7;
0; Mismatches 121;
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STRUCTURAL PROTEIN
CF75E75EFD8FBE2C
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CRC64;
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STRAIN=Neudoerf1;
MEDLINE=96036491; PubMed=7483260;
MEDLINE=96036491; PubMed=7483260;
Wallner G., Mandl C.W., Kunz C., Heinz F.X.;
"The flavivirus 3'-noncoding region: extensive size heterogeneity
independent of evolutionary relationships among strains of tick-borne
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88322870; PubMed=3413985;
Mandl C.W., Heinz F.X., Kunz C.;
"Sequence of the structural proteins of tick-borne encephalitis virus (western subtype) and comparative analysis with other flaviviruses.";
Virology 166:197-205(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 281-680.
MEDLINE=95272700; PubMed=7753193;
Rey F.A., Heinz F.X., Mandl C.W., Kunz C., Harrison S.C.;
"The envelope glycoprotein from tick-borne encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=90051080; PubMed=2554575;
Mandl C.W., Heinz F.K., Stoeckl E., Kunz C.;
"Genome sequence of tick-borne encephalitis virus (Western subtype)
and comparative analysis of nonstructural proteins with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Neudoerfl;
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[2]
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                                                                                                                                                                                                                                                                                                                                          EMBL; U27495; AAA86870.1; PIR; A31052; GNWVNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Neudoerfl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 767-3414 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flaviviruses.";
Virology 173:291-301(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3 and NS5 may play a role in the viral RNA replication. CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viprecursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {RNA}(N).
SUBUNIT: The virion of this virus is a nucleocapsid covered lipoprotein envelope. The envelope consists of two proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375:291-298(1995).
                                                                                                                           IPR000069;
IPR001157;
IPR000752;
IPR000487;
IPR000404;
IPR0001528;
                                                                                                                                                                                                                                  IPR009003;
IPR001410;
IPR001122;
IPR000336;
                                     IPR000208;
IPR002535;
IPR001650;
IPR007110;
IPR001850;
                                                                                                                                                                                                                                                                                                                         10-JUN-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otein envelope. The envelope consists of two proteins:

M and glycoprotein E. The nucleocapsid is a complex of c and mRNA.
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                                                               Flavi M.
Flavi MS1.
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Core protein; Coat protein;
ATP-binding; Transmembrane;
INIT_MET 1
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ProDom; PD001496; Flavi NS1; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01728; FtsJ; 1. Pfam; PF00271; helicase
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M00490; HELIC; 1.

PS00690; DEAH ATP HELICASE; FALSE NEG.

pS00690; DEAH ATP HELICASE; FALSE NEG.

psourcein; Grycoprotein; Transferase; RNA-directed RNA polymerase;

cein; Gote protein; Envelope protein; Hydrolase; Helicase;

otein; Coat protein; Envelope protein; 3D-structure.

ding; Transmembrane; Nonstructural protein; 3D-structure.

REMOVED FROM CAPSID PROTEIN C BY THE

CELLULARA AMINOPEPTIDASE.

1 112 CAPSID PROTEIN C.
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'AA; 1.
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i_NS5; 1.
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_helicase; 1.
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MAJOR ENVELOPE PROTEIN E.
MONSTRUCTURAL PROTEIN NS2A.
MONSTRUCTURAL PROTEIN NS2A.
MONSTRUCTURAL PROTEIN NS2B.
PROTEASE (MS3).
PROTEASE (MS3).
MONSTRUCTURAL PROTEIN NS4A.
MONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (INVOLVED IN FUSION.
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InterPro; [nterPro; [nterPro; InterPro; InterPro; [nterPro; (nterPro; InterPro; InterPro; InterPro; InterPro; PIR; A31052; PDB; 1SVB; 1

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RESULT 15
POLG TBEVS STANDARD; PRT; 3412 AA.
ID POLG TBEVS STANDARD;
AC P07720; P07721; Q88475; Q88476; Q88477; Q88478; Q88479; Q88877;
AC Q88878; Q88879; Q88879; DT 01-MAY-1991 (Rel. 07, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DT Genome polyprotein [Contains: Capsid protein C (Core protein);
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                 HLTPLQD-----WAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSA
                                                                                                                                                                                                               GSKGVLHT
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Pred. No. 47;
28; Mismatches
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          protein); Matrix
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           InterPro;
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InterPro;
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Yamshchikov V.F., Pletnev A.G.,
"Nucleotide sequence of the genome region
proteins and the NS1 protein of the tick k
Nucleic Acids Res. 16:7750-7750(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=90101381; PubMed=2136778;

Pletnev A.G., Yamshchikov V.F., Blinov V.M.;

Pletnev A.G., Yamshchikov V.F., Blinov U.M.;

"Nucleotide sequence of the genome and complete amino acid sequence
of the polyprotein of tick-borne encephalitis virus.";
                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein (Envelope protein M); Major envelope protein proteins NS1, NS2A, NS2B, NS4A and NS4B; Protease/Hel(EC 3.4.21.98) (NS3); RNA-directed RNA polymerase (EC (NS5)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-683 AND 777-1002 FROM N.A. MEDLINE=86220766; PubMed=3709796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology
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Flavivirus.
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      o; IPR009003; Cys_Ser_trypsin.
o; IPR001410; DEAD;
o; IPR001412; Flavi_capsidC.
o; IPR000336; Flavi_glycoprotE.
o; IPR000036; Flavi_NS1.
o; IPR0000752; Flavi_NS2A.
o; IPR000487; Flavi_NS2B.
o; IPR000447; Flavi_NS4B.
o; IPR0001528; Flavi_NS4B.
o; IPR0001528; Flavi_NS4B.
o; IPR0001538; Flavi_NS4B.
o; IPR001538; Flavi_NS4B.
o; IPR001538; Flavi_NS4B.
o; IPR001539; Flavi_NS4B.
o; IPR001539; Flavi_NS5.
o; IPR001550; Helicase_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encephalitis virus (strain Sofjin) (TBEV).
sRNA positive-strand viruses, no DNA stage; Flaviviridae;
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ALT_SEQ.
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ng as its content
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porne encephalitis virus
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ProDom; PD001496; Flavi NSI; 1.

PROSITE; PS00690; DEAH_ATP_HELICASE; FALSE_NEG.

POLYDrotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;

Core protein; Cost protein; Envelope protein; Hydrolase; Helicase;

ATP-binding; Transmembrane; Nonstructural protein.

INIT_MET 1 1 CELLULAR AMINOPEPTIDASE.

CHAIN 1 112 CAPSID PROTEIN C.
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Pfam; PF00271; helicase C; 1.
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Pfam; PF01003; Flavi
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1525 QRQVGVGYGSKGVLHT-----MWHVTRGAALSIDDAVAGP-----YWADVKEDVVCYGG 1573
                                            155 EVQV-VSTATQSFLATCVNGVCWTVFHGAG---SKTLAGPKGPITQMYTNVDQDLV----
                                                                                                                                             95 SGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEG
                                                                                                                                                                                         5.5%;
l Similarity 24.4%;
50; Conservation
                                                                                                ŚĠĹVFŚGQGĠŔĖRGDRPFEVKDĠV-YŔIFSP
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                                                                                                                                                                                                                                                                                     7 P1128 NONSTRUCTURAL PROTEIN NS 1358 NONSTRUCTURAL PROTEIN NS 2110 PROTEIN NS 2110 PROTEIN NS 2110 PROTEASE/HELICASE (NS3).

2110 PROTEASE/HELICASE (NS3).

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1122 PROTENTIAL.

259 POTENTIAL.

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NS4B; 1.
NS5; 1.
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MAJOR ENVELOPE PROTEIN NS1 (OR
NONSTRUCTURAL PROTEIN NS2A (O
NONSTRUCTURAL PROTEIN NS2B.
PROTEASE/HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED ENA POLYMERASE (
                                                                                                                                                                                                                      Score 87; DB
Pred. No. 58;
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                                                                   Pred. No. is the number of results predicted by chance to have, a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: sp_archea:*
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1589
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Query
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Copyright (c) 1993 - 2004 Compugen Ltd.
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No.	Score	Match	Length	BB.	ID	Description
1	1550	97.5	3010	12	Q9J3H7	Q9j3h7 hepatitis c
N	1545	97.2	3010	12	Q68826	٠,
ω	1545	97.2	3010	12	P90191	P90191 hepatitis c
4	1544	97.2	3010	12	Q9DTE6	•
5	1542	97.0	3010	12	Q9DTE4	Q9dte4 hepatitis c
6	1541	97.0	3010	12	Q9DTD6	
7	1540	96.9	3010	12	P88803	
8	1539	96.9	3010	12	Q9J3H5	Q9j3h5 hepatitis c
9	1539	96.9	3010	12	Q807P3	
10	1537	96.7	3010	12	Q9J3F9	w
11	1534	96.5	361	12	070815	070815 hepatitis c
12	1534	96.5	3008	12	Q9J3F4	Q9j3f4 hepatitis c
13	1534	96.5	3010	12	Q9J3H3	Q9j3h3 hepatitis c
14	1533	96.5	3010	12	Q9J3H2	••
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j3g3	9qiy4	9dte9	9qiy5	9j3i1	8qr18	9j3g6	9qp61	70818	9dte3	99au2	9dte0	9dtf0	9dtd7	99668	68788	81817	81755	9j3h4	9wmx2	9j3h9	91au0	9j3h6	9qix5	9qix6	9qiy8	9qiy7	09796
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GO; GO:0005489; F:electron transporter activity; IEA. GO; GO:0003723; F:RNA binding; IEA. GO; GO:000368; F:RNA-directed RNA polymerase activity; IEA. GO; GO:0008236; F:serine-type peptidase activity; IEA. GO; GO:0005198; F:structural molecule activity; IEA.	GO:0019031; GO:0005524; GO:0008026;	; PS0329; PS0329. iP; P26663; lJXP. GO:0016021; C:integr GO:0019028; C:viral	PIR; PQ0246; PQ0246. PIR; PQ0804; PQ0804.	C AND MRNA (BY SIMILARITY). 56; AAF65946.1;	PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A CONFLEX OF	Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. -!- SUBMINT: THE VIRION OF THIS VIRIS IS A NUCLEOCAPSID COVERED BY A	Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C.; "Characteristics of hepatitis C viral genome associated with disease	UENCE FROM N.A. AIN=MD15;	NOBICLETIES,	remove portyproceth. Hepatitis C virus. Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Henarivirus		ULT 1 3H7 Q9J3H7 PRELIMINARY; PRT; 3010 AA.

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RESULT 2
Q68826
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R Pfam; PF01539; HCV_env; 1.

R Pfam; PF01539; HCV_NS1; 1.

Pfam; PF01539; HCV_NS2; 1.

Pfam; PF01006; HCV_NS43; 1.

Pfam; PF01006; HCV_NS43; 1.

Pfam; PF01006; HCV_NS43; 1.

Pfam; PF01506; HCV_NS53; 1.

Pfam; PF01998; Viral RdPp.
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane. SEQUENCE 3010 AA; 327365 MW; D8653F7317FFA106 CRC64;
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InterPro;
       Q68826 PRELIMINARY;
Q68826;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
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IPR000345; CytC_heme_BS.
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P:viral transformation; IEA.
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P:proteolysis and pep
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HCV_core.
HCV_NS1.
HCV_NS2.
HCV_NS4a.
HCV_NS5a.
HCV_NS5a.
HCV_Rdsp.
HCV_Rdsp.
Peptidase_C29.
RNA_pol_DS_PS_RNA_pol_PS_vir
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2.2e-127;
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Query Match
Best Local Similarity
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Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01539; HCV_NS2; 1.
Pfam; PF01006; HCV_NS3a; 1.
Pfam; PF01006; HCV_NS3a; 1.
Pfam; PF01001; HCV_NS5a; 1.
Pfam; PF01001; HCV_NS5a; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00271; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; Coat Protein; Enve.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:000526; F:serine-type peptidase activity; IEA.
GO; GO:000526; F:serine-type peptidase activity; IEA.
GO; GO:000529; F:structural molecule activity; IEA.
GO; GO:000529; F:transferase activity; IEA.
GO; GO:000529; F:transferase activity; IEA.
GO; GO:000530; P:iranscription; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
GO; GO:0019079; P:viral transformation; IEA.
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Hepatitis C virus.
Viruses, ssRNA positive-strand viruses,
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NCBI_TaxID=11103;
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                                                                                          ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane. SEQUENCE 3010 AA; 327150 MW; 7270F47984554FAD CRC64;
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IPR001410; DEAD.
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HCV_core.
HCV_env.
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97.2%;
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Score 1545;
Pred. No. 6
   5; DB 12;
6.1e-127;
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                                Length 3010;
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RA Enomoto N., Sakuma I., Asahina Y., Kurosaki M., Murakami T.,

A Yamamoto C., Izumi N., Marumo F., Sato C.;

I' Comparison of full-length sequences of interferon-sensitive and

I'' Comparison of full-length sequences of interferon-sensitive and

I'' Comparison of full-length sequences of interferon-sensitive and

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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Hepatitis C virus.
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Enomoto N., Sakuma I., Asahina Y.,
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NCBI_TaxID=11103;
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InterPro; IPR001410; DEAD.
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GO:0006350; I
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yprotein; RNA-directed RNA p
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m; PF01542; HCV_core; 1.
m; PF01539; HCV_env; 1.
m; PF01538; HCV_WS1; 1.
m; PF01538; HCV_WS2; 1.
m; PF01006; HCV_WS2; 1.
m; PF01001; HCV_WS4a; 1.
m; PF01506; HCV_WS4a; 1.
m; PF01506; HCV_WS4a; 1.
m; PF01506; HCV_WS4a; 1.
m; PF01506; HCV_WS5a; 1.
m; PF0027; helicase_C; 1.
m; PF0029; Viral_RdRp; 1.
m; PF0099; Viral_RdRp; 1.
pr0; PD186062; HCV_WS1; 1.
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0; IPR00252; HCV_core.
0; IPR00251; HCV_env.
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0; IPR00251; HCV_NS4.
0; IPR001490; HCV_NS4b.
0; IPR001650; HCV_NS4b.
0; IPR001650; HCV_NS4b.
0; IPR001650; HCV_NS6b.
0; IPR001650; HCV_RGRP.
0; IPR001650; HCV_RGRP.
0; IPR001650; HCV_RGRP.
0; IPR001650; HCV_RGRP.
0; IPR001650; HCV_RGRP.
0; IPR001650; HCV_RGRP.
0; IPR001050; RNA_DOl_DS_PS.
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                       TMR 1206
                                                                                                              RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
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                                                                                                                                                                                        GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                      RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
                                                                                                                                                                                                                                                                         RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH 180
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P:viral transformation; IEA
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RNA polymerase; Transferase; Transmembrane.
CORE PROTEIN.
E1.
E2.
NS2.
NS2.
NS3.
NS4B.
NS4B.
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Pred. No. 6.1e-127;
8; Mismatches 4;
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01-MAR-2001
01-CCT-2003
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Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome polyprotein. Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
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PIR; A61196; A61196.
PIR; PS0329; PS0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000526; F:ATP binding; IEA.
GO; GO:0008026; F:ATP binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003968; F:scrune-type peptidase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
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                                                                                                                                                                                                                                                                                  PF01543;
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IPR002522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19079; P:viral genome replication; IEA.
19087; P:viral transformation; IEA.
IPR009003; Cys Ser trypsin.
IPR000345; CytC heme BS.
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                               HCV_core; 1, HCV_env; 1, HCV_NS1; 1, HCV_NS2; 1, HCV_NS3; 1, HCV_NS4a; 1, HCV_NS4a; 1, HCV_NS4a; 1, HCV_NS5a;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:transferase activity; IF P:electron transport; IEA. P:proteolysis and peptidol
                                                                                                                                                                                                                                                                                  _capsid;
                                                                                                                                                                                                                                                                                                                                                                                                                          HCV_capsid.
HCV_core.
HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS4a.
HCV_NS4a.
HCV_NS5a.
HCV_NS5a.
                                                                                                                                                                                                                                                                                                               Helicase C.
Peptidase C29.
RNA pol DS PS.
RNA pol PSvir.
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annotation update)
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EMBL; AB049093; BAB18806.1; -.

PIR; A61196; A61196.

PIR; PQ0246; PQ0246.

PIR; PQ0804; PQ0804.

PIR; PS0329; PS0329.

HSSP; P26663; JUXP.

GO; GO:0016021; C:integral to membrane; IE
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9DTE4; PRELIMINARY;
Q9DTE4;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00190; CYTOCHROME_C; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprote;
Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Transferase; Transmembrane
SEQUENCE 3010 AA; 327042 MW; 3807DC6879684C95 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00998; Viral RdRP;
ProDom; PD186062; HCV_NS1;
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                          Genome polyprotein.
Hepatitis C virus.
Viruses, sgRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi K., Iwat
Hatahara T., Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=HCVT150;
                                                                                                                                                                                                                                                                                                                                                       "Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLLAPITAYSQOTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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Ohta Y., Kanai K., Maruo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.2%;
95.7%;
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Last sequence update)
Last annotation update)
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Matsumoto H., H., Baba K., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 12;
7.4e-127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                                                                                                                                                                                                                                                                                              fifteen patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flaviviridae;
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InterPro; IPR007094; RNA pol PS
InterPro; IPR007094; RNA pol PS
Pfam; PF01543; HCV_core; 1.
Pfam; PF01543; HCV_core; 1.
Pfam; PF01543; HCV_NS1; 1.
Pfam; PF01563; HCV_NS2; 1.
Pfam; PF01563; HCV_NS2; 1.
Pfam; PF01561; HCV_NS4a; 1.
Pfam; PF01016; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS5a; 1.
Pfam; PF01071; helicase C; 1.
Pfam; PF00271; NelTone; 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_cove.
InterPro; IPR002519; HCV_env.
InterPro; IPR002519; HCV_NS1.
InterPro; IPR002519; HCV_NS2.
InterPro; IPR000745; HCV_NS4.
InterPro; IPR001490; HCV_NS4.
InterPro; IPR001490; HCV_NS4.
InterPro; IPR001650; HCV_NS6.
InterPro; IPR001650; Helicase_C29.
InterPro; IPR001650; Helicase_C29.
InterPro; IPR0017994; RNA_pol_pS_PS.
InterPro; IPR007994; RNA_pol_PS_VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00190; CYTOCHROME C; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 327324 MW; 3DE6CF249BD1151C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0019079; P:viral genome replication; IEA.
GO; GO:0019087; P:viral transformation; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO: 0003723;
GO: 0003968;
GO: 0008198;
GO: 0006198;
GO: 00066118;
GO: 00066118;
GO: 0006350;
GO: 0019079;
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GO:0008026;
GO:0005489;
                                                                                                                                                                                                                                                                                        964 LRDLAVAVEPVVFSDMETKIITWGADTAACGDIILGLPVSARRGKEILLGPADSLEGQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                             290;
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       TMR 303
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                                                                                     RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                             GAGSKTLAGFKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                              RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYH
                                                                                                                                                                                                                                            RLIAPITAYSQQTRGLIGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                             RRGDGRGS
                                                                                                                                     GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVR
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P:structural molecule activity; IEA.
P:transferase activity; IEA.
P:electron transport; IEA.
P:proteolysis and peptidolysis; IEA.
P:transcription; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:RNA binding; IEA.
F:RNA-directed RNA polymerase activity; IEA.
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95.7%;
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dependent helicase activity; IEA.
ctron transporter activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1542;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                             LLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
.1e-126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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   R HSSP, P26663; FD329.

R HSSP, P26663; IJXPP.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0008026; F:ATP binding; IEA.

R GO; GO:0005828; F:ATP binding; IEA.

R GO; GO:0005828; F:ATP binding; IEA.

R GO; GO:0005787; F:bydrolase activity; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0005198; F:serine-type peptidase activity; IEA.

R GO; GO:0005198; F:serine-type peptidase activity; IEA.

R GO; GO:0005198; F:serine-type peptidase activity; IEA.

R GO; GO:0005198; F:serine-type peptidase activity; IEA.

R GO; GO:0005198; F:serine-type peptidase activity; IEA.

R GO; GO:0005198; F:serine-type peptidase activity; IEA.

R GO; GO:0005198; F:serine-type peptidase activity; IEA.

R GO; GO:0005198; F:serine-type peptidase C.

R InterPro; IPR001251; HCV_NS5a.

R InterPro; IPR001256; HCV_NS5a.

R InterPro; IPR001266; HCV_NS5a.

R InterPro;
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     Pfam;
Pfam;
Pfam;
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Pfam;
Pfam;
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Q9DTD6;
01-MAR-2001
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi K., Iwata K.
Hatahara T., Ohta Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=HCVT221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepatitis C virus.
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repro; IPR007095; RNA po

repro; IPR007094; RNA po

pp01543; HCV capsid;

pp01542; HCV core; 1.

pp01539; HCV env; 1.

pp01536; HCV NS1; 1.

pp01536; HCV NS2; 1.

pp01538; HCV NS3; 1.

pp02907; HCV NS4a; 1.
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Y., Kanai K.,
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anai K., Maruo
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16,
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H., Baba K
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Baba K., Hijikata M.,
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Matches Query Match Best Local :

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ProDom; SMART; S

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Matches 291
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SMART; S
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ATP-binding; Coat protein; Envelope protein; Glycoprotein;
Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 327108 MW; DE182D810EF78EE4 CRC64;
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Pfam;
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                                  MEDINE-9530824; PubMed=7542279;
MEDINE-9530824; PubMed=7542279;
Enomoto N., Sakuma I., Asahina Y., Kurosaki M., Murakami T.,
Yamamoto C., Izumi N., Marumo F., Sato C.;
Yamamoto C., Izumi N., Marumo F., Sato C.;
"Comparison of full-length sequences of interferon-sensitive and resistant hepatitis C virus 1b.";
J. Clin. Invest. 96:224-230(1995).
-i- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE MUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).
EMBL, D50484; BAA09075.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03,
01-MAY-1997 (TrEMBLrel. 03,
01-OCT-2003 (TrEMBLrel. 25,
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NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=HCV-1b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses,
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Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                           STRAIN=HCV-1b;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Enomoto
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hes 291;
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n; PF01506; HCV_NS5a; 1.
n; PF00271; helicase C; 1.
n; PF00998; Viral_RdRP; 1.
om; PD186062; HCV_NS1; 1.
UT; SM00487; DEXDC; 1.
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                  A61196; A61196.
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Pred. No. 1.
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Matches 289;
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InterPro; IPRO07095; RNA_Dol_PSvir.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01549; HCV_env; 1.
Pfam; PF01559; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF01006; HCV_NS3; 1.
Pfam; PF01001; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00271; helicase_C; 1.
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G0; G0:0019031; C:vi
G0; G0:0008026; F:AII
G0; G0:0008026; F:AII
G0; G0:0003723; F:AII
G0; G0:0003828; F:EX
G0; G0:0005198; F:SE
G0; G0:0005198; F:SE
G0; G0:0016740; F:SE
G0; G0:00065508; F:SE
G0; G0:00065508; F:SE
G0; G0:00065508; F:SE
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA directed RNA polymerase activity; IEA.
GO; GO:0003236; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005236; F:serine-type peptidase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:stransferase activity; IEA.
GO; GO:0006508; P:transferase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                      Polyprotein;
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                            1024
                                                                                    964
                                                                                                                                           904
 181
                                                        121
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                                                                                                                                                                                                                  Similarity
                                                                                                     LRDLAVAVEPVTFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW
                                                                                                                                                               AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALIGTYVVDHLTPLQDWAHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002522;
IPR002521;
IPR002519;
IPR002531;
IPR002531;
GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                         RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
                                                                                   LRDLAVAVEPVVFSDMETKIITWGADTAACGDIISGLFVSARRGREILLGFADSFEGOGW
                                                                                                                                           RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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IPR001410;
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384
810
1027
1658
1712
1973
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                       , Envelope protein; Glycoprotein; Nonstructural protein; RNA-directed RNA polymerase; Transferase; Transmembrane
1 191 CORE PROTEIN.
                                                                                                                                                                                                                                                           AA;
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809
1026
1657
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1972
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HCV core.
HCV env.
HCV NS2.
HCV NS2.
HCV NS4a.
HCV NS5a.
HCV NS5a.
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E2.
NS2.
NS4A.
NS4B.
NS5A.
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Pred. No. 1.7e
9; Mismatches
                                                                                                                                                                                                                                                                            NS5B
                                                                                                                                                                                                                                                            5F81505783FEFFB8 CRC64;
                                                                                                                                                                                                   1.7e-126;
ches 5;
                                                                                                                                                                                                                                 DB 12;
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                                                                                                                                                                                                      Indels
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                                 1083
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CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY A CC PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: CC PROTEIN C AND MENA (BY SIMILARITY).

DR EMBL, AF207758; AAF65948.1; -.

DR PIR; P00246; P00246.

R PIR; P00254; P00254.

R PIR; P27958; 1HEI.
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InterPro;
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InterPro;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:electron transporter activity; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003568; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:transferase activity; IEA.
GO; GO:0005198; F:electron transport; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0005509; P:transcription; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepacivirus.
NCBI_TaxID=11103;
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                                                                       IPR00149
IPR00286
IPR00216
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IPR00251
IPR00074
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IPR000345; CytC_hem
                                                                                                                                                                                                                     IPR00252
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(TremBLrel. 15, Last seq
(TremBLrel. 25, Last ann
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    HCV capsid.
HCV core.
HCV env.
HCV NS1.
HCV NS2.
HCV NS4a.
HCV NS5a.
HCV NS5a.
HCV RdRP.
HCL Rdse C.
Peptidase C29.
RNA pol_D5_PS.
                                                                                                                                                                                                                                                                            Ser_trypsin.
C_heme_BS.
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        no DNA stage; Flaviviridae;
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disease
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QRESULT

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SEQUENCE FROM N.A.

STRAIN=MILE;

STRAIN=MILE;

KISHINB=22047193; PubMed=12051758;

KiSHINB=42047193; PubMed=12051758;

KiSHINB=42047193; PubMed=12051758;

Nio Y: Hosaka M., Miyanari Y., Shimotohno K.;

Nio Y: Hosaka M., Miyanari Y., Shimotohno K.;

"Subgenomic replicon derived from a cell line infechepatitis C virus.";

hepatitis C virus.";

Biochem. Biophys. Res. Commun. 293:993-999(2002).

EMBL; AB080299; BAC54896.1; -

GO; GO:0019038; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.
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Viruses; ssRNA positive-strand viruses, Hepacivirus.

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DNA stage; Flaviviridae;

line infected

Takahashi H.,

Noshi

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NCBI_TaxID=11103;

Hepatitis C virus.

Last Last

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Best Local :
Q807P3;
01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-CCT-2003 (TrEMBLrel.
                                                Q807P3
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Pfam;
Pfam;
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Pfam; PF01543;
Pfam; PF01542;
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Pfam;
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PF00271; helicase C; 1.
PF00998; Viral RdRP; 1.
m; PD186062; HCV_NS1; 1.
7; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                           290;
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                                                                                                         TMR
                                                                                                                                                                                                                   GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                                               RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                                                                                              景
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                                               PRELIMINARY;
                                                                                                                               303
                                                                                                                                                                                                                                                                                                                                                                                                       96.9%;
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Pred. No. 2.1e-126;
7; Mismatches 6;
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Best Local S
Matches 291
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InterPro; IPR000345; CytC heme_BS.
InterPro; IPR0003410 DEAD.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_capsid.
InterPro; IPR002519; HCV_env.
InterPro; IPR002519; HCV_NS1.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR001690; HCV_NS5a.
InterPro; IPR001650; H
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Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01568; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS4b; 1.
Pfam; PF00271; helicase_C; 1.
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SEQUENCE 3010 AA;
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GO:0005489
GO:0003783
GO:0003783
GO:0008236
GO:00065198
GO:00065198
GO:0006508
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SM00487; DEXDC;
SM00490; HELICC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                     RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                                                                                                                                                            GAGSKTLAGPKGPITOMYTNVDODLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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(6; F:ATP dependent helicase activity; IEA.
19; F:electron transporter activity; IEA.
13; F:RNA binding; IEA.
16; F:RNA-directed RNA polymerase activity; IEA.
16; F:serine-type peptidase activity; IEA.
18; F:structural molecule activity; IEA.
18; F:structural molecule activity; IEA.
19; P:proteolysis and peptidolysis; IEA.
10; P:transcription; IEA.
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P:viral transformation; IEA.
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RESULT 10
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RI Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC ILIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
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01-OCT-2000
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InterPro;
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Hepatitis C virus.
Viruses; ssRNA positive-strand
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| IPR009003; Cys Ser_trypsin.
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| IPR000345; CytC heme BS.
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| IPR002521; HCV_capsid.
| IPR002521; HCV_capsid.
| IPR002531; HCV_NS1.
| IPR002531; HCV_NS4.
| IPR002531; HCV_NS4.
| IPR002166; HCV_NS48.
| IPR002166; HCV_NS48.
| IPR002166; HCV_NS48.
| IPR002166; HCV_NS48.
| IPR002166; HCV_NS48.
| IPR002165; HCITABSE_C.
| IPR002165; HCITABSE_C.
| IPR007094; RNA_pol_DS_PS.
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"Enzymatic characterization of purified NS3 serine prolematics C virus expressed in Escherichia coli.";
FEBS Lett. 378.33-42(1998).
EMBL; AB013620; BAA28498.1; -.
HSSP; P27958; 1HEI.
GG; GO:0006236; F:serine-type peptidase activity; IEA.
GG; GO:0006508; P:proteolysis and peptidolysis; IEA.
GG; GO:0006508; P:viral transformation; IEA.
GG; GO:019087; P:viral transformation; IEA.
InterPro; IPR009103; Cys.Ser_trypsin.
InterPro; IPR0092518; HCV_NS2.
InterPro; IPR004109; Peptidase_C29.
Pfam; PF01538; HCV_NS2; 1.
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070815;
01-AUG-1998
01-AUG-1998
01-OCT-2003
                                                                                                                                                                                       Yamada K., Mo.
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                                                                                                                                                              Virology
[2]
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Hepatitis C virus.
Viruses; SSENA positive-strand
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                                                                                                                               Miyamura T.;
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Best Local S
Matches 288
R EMBL; AF208024; AAF61205.1; -.

R PIR; A61196; A61196.

R PIR; P00246; P00246.

R PIR; P00229; P50329.

R HSSP; P28663; JJXP.

R GO; GO:0016021; C:viral capsid; IEA.

GO; GO:0019031; C:viral capsid; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0019031; F:ATP binding; IEA.

R GO; GO:0005524; F:ATP dependent helicase activity; IEA.

R GO; GO:0008026; F:ATP dependent helicase activity; IEA.

R GO; GO:0008727; F:HNA binding; IEA.

R GO; GO:0003727; F:HNA binding; IEA.

R GO; GO:0003727; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003726; F:SENA-directed RNA polymerase activity; IEA.
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Submitted (NOV-1999) to the
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LIPOPROTEIN ENVELOPE. TH
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01-OCT-2000 (TremBLrel.
01-OCT-2003 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
Viruses; ssRNA positive-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9J3F4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C. "Characteristics of hepatitis C viral genome associated with disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MD34;
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                                                                                                                                                                                                                                                                                                                                                         mitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY LIPOPROTEIN ENVELOPE: THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLECCAPSID IS A COMPLEX OF PROTEIN C. AND MENA (BY SIMILARITY).
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Pfam; PF00998; Viral RdRP; 1.
ProDom; PD186062; HCV_NSI; 1.
SMART; SM00487; DEXDC; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3008 AA; 326834 MW; 99AE09E14C3109F4 CRC64;
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m; PF01542; HCV_core; 1.
m; PF01539; HCV_env; 1.
m; PF01560; HCV_NS1; 1.
m; PF01560; HCV_NS3; 1.
m; PF01006; HCV_NS3; 1.
m; PF01006; HCV_NS4a; 1.
m; PF01506; HCV_NS5a; 1.
m; PF01506; HCV_NS5a; 1.
m; PF00271; helicase_C; 1.
m; PF00998; Viral_RdRP; 1.
Dom; PD0186062; HCV_NS1; 1.
T; SM00487; DEXDC: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:structural molecule activity; IEA. F:transferase activity; IEA. P:electron transport; IEA. P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P:transcription;
                                                                                    LLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV core.
HCV env.
HCV NS1.
HCV NS1.
HCV NS4.
HCV NS48.
HCV NS48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicase C.
Peptidase C29.
RNA pol DS PS.
RNA pol PSvir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.5%;
                                                                                                                                                                      :TQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVR
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Pred. No. 5.7e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
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RESULT 13 Q9J3H3

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R Pfam; PF01543; HCV_CORPIC;

R Pfam; PF01539; HCV_ENV; 1.

R Pfam; PF01539; HCV_MS1; 1.

R Pfam; PF01506; HCV_MS1; 1.

R Pfam; PF01066; HCV_MS3; 1.

R Pfam; PF01006; HCV_MS4; 1.

R Pfam; PF01006; HCV_MS4a; 1.

R Pfam; PF01006; HCV_MS4a; 1.

R Pfam; PF01071; halicase_C; 1.

R Pfam; PF00271; halicase_C; 1.

R Pfam; PF00998; Viral RdRP; 1.

DR Pfam; PF00998; Viral RdRP; 1.

DR ProDom; PD186062; HCV_NS1; 1.

DR PROSITE; PS00190; CTV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9J3H3;
Q9J3H3;
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome polyprotein.
Hepatitis C virus.
Viruses; seRNA positive-strand
                                                                                                                                        Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
Pfam;
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF207760; AAF65950.1; -. PIR; A61196; A61196. PIR; PS0329; PS0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016508; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003968; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:00065198; F:rransferase activity; IEA.
GO; GO:0006508; P:proteclysis and peptidolysis; IEA.
GO; GO:0006508; P:transcription; IEA.
GO; GO:0006508; P:transcription; IEA.
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"Characteristics of hepatitis C viral genome associated
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                                                                                                                                                                                                                                                                                                                                   | IPR002522; HCV capsid. | IPR002521; HCV core. | IPR002531; HCV env. | IPR002531; HCV NS1. | IPR002531; HCV NS2. | IPR002531; HCV NS4a. | IPR002516; HCV NS4b. | IPR002566; HCV NS4b. | IPR002566; HCV NS5a. | IPR002166; NNA DO1 DS PS. | IPR002096; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS PS. | IPR002094; NNA DO1 DS 
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IPR002522;
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RESULT RESULT REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
RA Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C RT "Characteristics of hepatitis C viral genome associated with disease RT progression.";

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ databases.

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ databases.

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ databases.

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CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ databases.

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ covERBD BY A NUCLECCAPSID COVERED BY A CC EMBL; AF207761; AAF265951.1; -.

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ IS A COMPLEX OF TWO PROTEINS:

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ IS A COMPLEX OF TWO PROTEINS:

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ IS A COMPLEX OF TWO PROTEINS:

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ IS A COMPLEX OF TWO PROTEINS:

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CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ IS A COMPLEX OF TWO PROTEINS:

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ IS A COMPLEX OF TWO PROTEINS:

CC cisumitted (Nov-1999) to the EMBL/GenBank/DDBJ IS A COMPLEX OF TWO PROTEINS:

CC cisumitted (Nov-1998) protecolysis and peptidolysis; IEA.

DR GO; GO:0006518; P:transcription; IEA.

DR GO; GO:0006529; P:transcription; IEA.
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Q9J3H2;
O1-OCT-2000 (TIEMBLICEL 1
01-OCT-2000 (TIEMBLICEL 1
01-OCT-2003 (TIEMBLICEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome polyprotein.
Hepatitis C virus.
Viruse; ssRNA positive-strand
Hepacivirus.
NCBI TaxID=11103;
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286; Conserv
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Pred. No. 5.7e-126;
1; Mismatches 6;
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Matches 288
         Q9J3IO PRELIMINARY;
Q9J3IO;
01-CCT-2000 (TrEMELrel. 1
01-CCT-2000 (TrEMELrel. 1
01-CCT-2003 (TrEMELrel. 2
Genome polyprotein.
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GO; GO:001:
InterPro;
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SMART; SM00487; DEXDC;
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InterPro; IPRO02522; HCV_capsid.
InterPro; IPRO02521; HCV_core.
InterPro; IPRO02521; HCV_core.
InterPro; IPRO02513; HCV_sore.
InterPro; IPRO02513; HCV_sore.
InterPro; IPRO02513; HCV_NS1.
InterPro; IPRO02513; HCV_NS4.
InterPro; IPRO00745; HCV_NS48.
InterPro; IPRO01490; HCV_NS48.
InterPro; IPRO0166; HCV_RdRP.
InterPro; IPRO01650; Helicase C.9.
InterPro; IPRO01799; RNA_DO1_DS_PS.
InterPro; IPRO07099; RNA_DO1_PSVir.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_NS2; 1.
Pfam; PF01539; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF00998; Viral_RdRP; 1.
Pfam; PF00998; Viral_RdRP; 1.
Pfam; PF00998; Viral_RdRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00190; CYTOCHROME C; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane
SEQUENCE 3010 AA; 326763 MW; 1A48EE4BE51440D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0019079; P:viral genome replication; GO:0019087; P:viral transformation; IEA. erPro; IPR009003; Cys Ser_trypsin. erPro; IPR000345; CytC heme_BS.
RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                                      GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                                                          RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
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                                                                                                          GAGSKALAGQKGPVTQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVR
                                                                                                                                                                                                           RLLAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYH
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95.0%;
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Pred. No. 7e-126;
9; Mismatches
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Last Last

sequence update) annotation updat

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Pfam; PF01539; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01001; HCV_NS4; 1.
Pfam; PF01001; HCV_NS4; 1.
Pfam; PF01506; HCV_NS5a; 1.
PFam; PF00271; helicase C; 1.
Pfam; PF00398; Viral_RdRP; 1.
PF000m; PD186062; HCV_NS1; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein; Hydrolase; Nonstructural protein; Polyprotein; RNA,-directed RNA polymerase; Transferase; Transmembrane.
RNA,-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 326692 MW; 074098DB305AF1A9 CRC64;
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Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F.,
"Characteristics of hepatitis C viral genome associated with o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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InterPro;
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PIR; A61196; A61196

PIR; PQ0246; PQ0246

PIR; PS0329; PS0329.

HSSP; P26663; 1JXP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                progression."
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NCBI_TaxID=11103;
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GO: GO:0019028; C:viral capsid; IEA.
GO: GO:0019031; C:viral capsid; IEA.
GO: GO:0019031; C:viral envelope; IEA.
GO: GO:0005224; F:ATP binding; IEA.
GO: GO:0005224; F:ATP binding; IEA.
GO: GO:0005489; F:electron transporter activity; IEA.
GO: GO:0005787; F:hydrolase activity; IEA.
GO: GO:0003723; F:ENA binding; IEA.
GO: GO:0003723; F:ENA binding; IEA.
GO: GO:0003963; F:ENA binding; IEA.
GO: GO:0003963; F:ENA binding; IEA.
GO: GO:0008236; F:SETHE-type peptidase activity; IEA.
GO: GO:0005198; F:structural molecule activity; IEA.
GO: GO:0005198; F:structural molecule activity; IEA.
GO: GO:0005198; F:structural molecule activity; IEA.
GO: GO:0006118; P:electron transport; IEA.
GO: GO:0006198; P:proteolysis and peptidolysis; IEA.
GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
GO: GO:0006309; P:transcription; IEA.
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                                                                                                                                                                                                                                                                                                                                                                   IPR00251
IPR00251
IPR00074
IPR00149
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IPR00252
IPR00251
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9079; P:viral genome replication; IEA.
9087; P:viral transformation; IEA.
IPR009003; Cys Ser trypsin.
IPR000345; CytC_heme_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:RNA-directed RNA polymerase activity, IEA.
                                                                                                                                                                                                                                                              _capsid;
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                                                                                                                                                                                                                                                                                                                                                    HCV_capsid.
HCV_core.
HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS4a.
HCV_NS4b.
                                                                                                                                                                                                                                                                        Peptidase C29.
RNA pol DS PS.
RNA pol PSvir.
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ctivity; IEA.
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Query Match

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1204
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                                                                      RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                        GAGSKTLAGÞKGÐITQMYTNVDQDLVGWQAÐÐGARSMTÐCTCGSSDLYLVTRHADVIÐVR
                                                                                                                              GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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                                                     RRGDGRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMET
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6; Mismatches
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Search completed: May 6, 2004, 09:35:45 Job time: 29:339 secs

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Minimum
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Listing first 45 summaries
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Match
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1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/FCTUS_COMB.pep:*
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US-09-919-901-2
US-09-919-901-11
US-09-919-901-11
US-09-919-901-33
US-09-919-901-33
US-09-263-933-11
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US-09-315-8501-12
US-08-384-616-12
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TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences,
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 1199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 2201
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-539-601-6
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US-09-539-601-6
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Sequence 12, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 2, Appli	equence	2	Sequence 14, Appl	Sequence 2, Appli	4	Sequence 2, Appli	Sequence 14, Appl	Sequence 2, Appli	-	9	Sequence 36, Appl	`	-

ALIGNMENTS

Sequence 6, Application US/09539601C Patent No. 6630343 GENERAL INFORMATION:

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Pred. No. 2.5e-144;
8; Mismatches 7;
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Length 2201;

RESULT

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Sequence 15. Application US/09539601C

Sequence 15. Application US/09539601C

Patent No. 6630343

GENERAL INFORMATION:
APPLICANT: Bartenschlager, Ralf FW

TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REPERENCE: all sequences
CURRENT APPLICATION NUMSER: US/09/539,601C

CURRENT FILING DATE: 2001-08-30

EARLIER FILING DATE: 199-04-03

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PATENTING Ver. 2.1

SEQ ID NO 15

LENGTH: 2201

TYPE: PRT

ORGANISM: Hepatitis C virus

US-09-339-601-15
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                                                                                                                  ; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3010
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-539-601-3
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Best Local S
Matches 288
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APPLICANT: Bartenschlager, Ralf FW
APPLICANT: INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEC ID NOS: 51
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                                            Query Match
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Matches 288; Conserv
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Local Similarity 95.0%;
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                                              Conservative
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Pred. No. 2.5e-144;
8; Mismatches 7;
                                          Score 1530; DB 4;
Pred. No. 3.9e-144;
8; Mismatches 7;
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APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION UMBER: 195 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER: OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 3010
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US-09-539-601-21
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                                                                                                                                        GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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Pred. No. 3.9e-144;
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US-09-539-601-27
; Sequence 27, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:

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US-09-263-933-4
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                                                                                                                      GENERAL INFORMATION:
APPLICANT: POCTS, KAZEN E.
APPLICANT: JOCKSON, ROBERTA L.
APPLICANT: JOCKSON, ROBERTA L.
APPLICANT: PATICK, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 4
SEQ ID NOS: 33
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Patent No. 6280940
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LENGTH: 3010
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Best Local Similarity
  Query Match
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TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
NUMBER OF SEQ ID NOS: 51
NUMBER: Patentin Ver. 2.1
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                                         LENGTH: 1692
TYPE: PRT
ORGANISM: Artificial Sequence
-09-263-933-4
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96.1%;
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Pred. No. 3.9e-144;
8; Mismatches 7; Indels 0
  Score 1527;
  DB 3;
Length 1692;
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CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/23,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
I NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
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Matches 286; Conserv
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Patent No. 6599738
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Best Local
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APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                   LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW 120
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GAGSKTLAGPKGPITQNYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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94.4%; Pred. No. 3.5e-144;
tive 11; Mismatches 6;
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Sequence 2, Application US/09263933

Patent No. 6280940

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jockson, Roberta L.

APPLICANT: Jackson, Roberta For USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/263,933

CURRENT FILING DATE: 1998-08-08

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEO ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEO ID NO 2

LENGTH: 2307

TYPE: PRT

ORGANISM: Artificial Sequence

US-09-263-933-2
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US-09-263-933-2
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Sequence 2, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
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Best Local :
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Local Similarity 94.4%; Pred. No. 5.4e-144;
Les 286; Conservative 11: Mismarch.
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FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER: 09 SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-263-933-11
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; OTHER INFORMATION:
US-09-919-901-2
                                                                                                                                     APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0

LENGTH. 1602
Query Match 95.9%; Score 1524; DB 3;
Best Local Similarity 94.1%; Pred. No. 6.9e-144;
Matches 285; Conservative 12; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6280940 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11,
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                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 11, Application US/09919901

| Sequence 11, Application US/09919901
| Patent No. 6599738
| GENERAL INFORMATION:
| APPLICANT: Potts, Karen E. APPLICANT: Jackson, Roberta L. APPLICANT: Jackson, Roberta L. APPLICANT: Patick, Amy X.
| APPLICANT: Patick, Amy X. TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A CURRENT APPLICATION NUMBER: US/09/919,901
| CURRENT FILING DATE: 1201-08-02 PRIOR FILING DATE: 1209-02-08 PRIOR APPLICATION NUMBER: 09/263,933 PRIOR FILING DATE: 1998-08-05 NUMBER: 09/279,611 PRIOR FILING DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-08-05 NUMBER: 07/28, PATENTAL DATE: 1998-0
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US-09-919-901-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.9%; Score 1524; DB 4; Length 1692; Best Local Similarity 94.1%; Pred. No. 6.9e-144; Matches 285; Conservative 12; Mismatches 6; Indels 0
                                                                                                                                  61 LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGQGW 120
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                           GAGSKTLAGPKGPITOMYTNVDODLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR 240
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Patent No. 6280940

Patent No. 6280940

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INH.BITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-00058

CURRENT APPLICATION NUMBER: US/09/263,933

CURRENT FILING DATE: 1999-03-08

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO SEQ ID NOS: 33

CORGANISM: Artificial Sequence

US-09-263-933-9
RESULT 13
US-09-919-901-9
; Sequence 9, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
; TITLE OF INVENTION: REFORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
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PRIOR FILING DATE: 1999-02-08
PRIOR PRIOL NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 2307
                                                                                                                                                              ; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 33; LENGTH: 3010; TYPE: PRT; ORGANISM: Hepatitis C virus US-09-539-601-33
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US-09-539-601-33
; Sequence 33, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
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                                                                                                          Query Match
Best Local S
Matches 287
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Best Local Similarity
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TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
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ORGANISM: Artificial Sequence
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          LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRGREILLGPADNFEGOGW
                                                                    AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
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94.1%; Pred. No. 1.
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                                                                                                        Score 1523; DB 4;
Pred. No. 2e-143;
8; Mismatches 8;
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1.1e-143;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta C.
APPLICANT: Jackson, Roberta C.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
FARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 1692
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US-09-263-933-18
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Best Local Similarity
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TMR
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                                 TMR
                                                                                RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                                                                             GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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US-10-650-585-13
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Sequence 11, Appli
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Indels 0; Gaps 0; JTGTYVYDHLTPLQDWAHAG 60	ngth 303;	Sequence 18, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appl Sequence 2, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

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; TYPE: PRT
; ORGANISM: HCV
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Sequence 4, Application US/10017736
Publication No. US20020192640A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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Best Local
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CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
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Pred. No. 1.5e-154;
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CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 4
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; TYPE: PRT
; ORGANISM: HCV
US-10-650-585-4 ·
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; ORGANISM: HCV
US-10-017-736-4
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Best Local Simi
Matches 303;
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Publication No. US20040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3
FILE REFERENCE: 13/082
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NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Similarity 100.0%; Pred. No. 1.7e-154;
03; Conservative 0; Mismatches 0;
RLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFH
                                                            LRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLEVSARRGREILLGPADNFEGQGW
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Pred. No. 1.7e-154;
; Mismatches 0;
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Matches
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CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 341
Sequence 14, Application US/10650585
Publication No. US20040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
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Publication No. US20020192640A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
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nes 303; Conserv
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US-10-017-736-13

VS-10-017-736-13

Sequence 13, Application US/10017736

Publication No. US20020192640A1

GENERAL INFORMATION:

APPLICANT: Beckringer Ingelheim (Canada) Ltd.

TITLE OF INVENTION: Purified Active HCV NS2/3 Profile REFERENCE: 13/082

CURRENT APPLICATION NUMBER: US/10/017,736

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/556,031

PRIOR FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 21

SEQ ID NO 13

SEQ ID NO 13

SEQ ID NO 13

SEQ ID NO 13

LENGTH: 352

TYPE: PRI
CRAMNISM: HCV

US-10-017-736-13
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CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR TILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 341
TYPE: PRT
ORGANISM: HCV
US-10-650-585-14
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Best Local Similarity 100.
Matches 303; Conservative
                                                                                                                            Query Match 100.0%; Score 1589; DB 13; Best Local Similarity 100.0%; Pred. No. 1.8e-154; Matches 303; Conservative 0; Mismatches 0;
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                                                                               AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG
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                                                                                                                                                                 DB 13; Length
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APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
1 SEQ ID NO 13
RESULT 9
US-10-017-736-12
(, Sequence 12, Application US/10017736
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US-10-650-585-13
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TYPE: PRT
ORGANISM: HCV
IS-10-650-585-13
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Publication No. US20040077066A1
GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 100.0%; Score 1589; DB 16;
Similarity 100.0%; Pred. No. 1.8e-154;
03; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LEIGHT: 380
TYPE: PRT
ORGANISM: HCV
US-10-650-585-12
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GENERAL INFORMATION:
APPLICANT: Boshringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Pro-
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
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US-10-650-585-12
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US-10-017-736-12
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Publication No. US20040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
APPLICANT: Briffied Active HCV NS2/3 Protease
                                    Best Local
Matches 3
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Best Local Similarity 100.
Matches 303; Conservative
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                                                                      Query Match
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 1 AGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGTYVYDHLTPLQDWAHAG 60
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                                    Score 1589; DB 16;
Pred. No. 2e-154;
Mismatches 0;
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Sequence 11, Application US/10017736

Publication No. US20020192640A1

GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082

CURRENT APPLICATION NUMBER: US/10/017,736

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/256,031

PRIOR APPLICATION NUMBER: 60/256,031

PRIOR APPLICATION NUMBER: 60/256,031

PRIOR FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSEQ for Windows Version 4.0

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US-10-017-736-11
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Matches
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ORGANISM: HCV
S-10-017-736-11
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                                                                  RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
TMR 393
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Sequence 2, Application US/10017736
; Sequence 2, Application US/20020192640A1
; GENERAL INFORMATION: US20020192640A1
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; APPLICANT: Boehringer Ingelheim (Canada) Ltd.
; TITLE OF INVENTION: Purified Active HCV NS2/3 Frotease
; FILE REFERENCE: 13/082
; CURRENT APPLICATION NUMBER: US/10/017,736
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/256,031
; PRIOR APPLICATION NUMBER: 60/256,031
; PRIOR TILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: HCV
US-10-017-736-2
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Publication No. US20040077066A1

GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Profile REFERENCE: 13/082

CURRENT APPLICATION NUMBER: US/10/650,585

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: US/10/017,736A

PRIOR FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/256,031

PRIOR FILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 21

SOTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 393

TYPE: PRT

ORGANISM: HCV

US-10-650-585-11
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Best Local Similarity 100.
Matches 303; Conservative
Query Match
Best Local Similarity
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100.0%;
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  Score 1589; DB 13;
Pred. No. 2.3e-154;
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; LENGTH: 409
; TYPE: PRT
; ORGANISM: HCV
US-10-650-585-2
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CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR PILING DATE: 2000-12-15
NUMBER: OF SEQ ID NOS: 21
SOPTWARE: FastSEQ for Windows Version 4.0
SBQ ID NO 2
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US-10-650-585-2
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 303;
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Publication No. US20040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION; Purified Active HCV NS2/3 Protease
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                            RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
                                                                      GAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVR
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       RRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMET
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Sequence 18, Application US/10017736

Publication No. US20020192640A1

GENERAL INFORMATION:
APPLICANT: Boshringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 PRICE REFERENCE: 13/082

FILE REFERENCE: 13/082

CURRENT APPLICATION NUMBER: US/10/017,736

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: 60/256,031

PRIOR TILING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 21

SOFFWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGTH: 303

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ALIGNMENTS

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AC HCV; enzyme; protease; NS2/3 (815-1206); hepatitis C virus inrechronic liver disease; cirrhosis; end-stage liver disease; virus hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein. ABG32184 standard; protein; 05-NOV-2002 ABG32184; 20-JUN-2002 WO200248375-A2. Hepatitis C virus. HCV protease NS2/3 truncation mutant 815-1206. (first entry) NS2/3 (815-1206); hepatitis C virus infection; cirrhosis; end-stage liver disease; virucide; 393 8

13-DEC-2001; 2001WO-CA001796.

15-DEC-2000; 2000US-0256031P.

(BOEH) BOEHRINGER INGELHEIM CANADA LTD.

Lamarre D,

Maurice R,

Pilote Ļ

Pause

WPI; 2002-599511/64.

Thibeault D,

Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.

Claim 41; Page 59-60; 67pp; English.

The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal residue amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length NS2/3 protease. Also included are (1) a composition (C) comprising an isolated HCV NS2/3 protease selected from full length NS2/3 protease, and isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a mutated sequence, where the protease is in a solution comprising a sufficient concentration of lawy Ndiethylamine oxide (LDAO) comprising a sufficient concentration of lauryldiethyl inhibitory peptide

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RESULT 2
ABG32181
ID ABG32181
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DT 05-N
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HCV
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KW hepp
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Best Local
                    HCV; enzyme; protease; NS2/3 (810-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO;
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                                                                                                           HCV protease
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                                                                                                                                                                                                                                      ABG32181 standard; protein; 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
                                                                                                                                                                                                                                                                                                                                                                                      GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGFKGFITQMYTNVDQDLVGWQA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 AA;
                                                                                                                                                                                                                                                                                                                                                   GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR
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                                                                                                           NS2/3
                                                                                                                                                      (first entry)
                                                                                                             (810-1206).
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Pred. No. 7.1e-191;
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Query Match
Best Local S
Matches 393
                                                                                                                                                                                                        Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
Synthetic.
                                                                                                                                                                                               Claim 42; Fig 1B; 67pp; English.
                   Sequence
                                                                                                                                                                                                                                           Thibeault D,
                                                                                                                                                                                                                                                             15-DEC-2000; 2000US-0256031P
                                                                                                                                                                                                                                                                       13-DEC-2001; 2001WO-CA001796
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                                                                                                                                                                                                                                                                                                        Peptide
                             terminal streptavividin tag
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                                                                                                                                                                                                                                                    BOEHRINGER INGELHEIM CANADA LTD.
     Similarity
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                    Ŗ,
                                                                                                                                                                                                                                           Lamarre
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398. .409
/note= "Streptavidia
     100.0%;
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                                                                                                                                                                                                                                                                                                    "Streptavidin
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     Score 2053; DB 5;
Pred. No. 7.6e-191;
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The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal residue amino acid 810 to 906, or having a minimal amino acid sequence, from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length NS2/3 protease. Also included are (1) a composition (C) comprising an isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a mutated sequence, where the protease is in a solution comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) to prevent auto-cleavage of the protease, (2) a NS2/3 inhibitory peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCV; enzyme; protease; NS2/3 (827-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide for screening inhibitors of non-structural proteases l as therapeutic agents against hepatitis C virus, comprises full h non-structural protease, or its truncation.
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16-OCT-2003 14-NOV-1996 AAR82694;

(revised)

entry)

AAR82694

standard;

protein;

3010

proteinase; hepatitis C virus; identification; cleavage.

inhibitor; proteolytic;

Partial HCV non-structural polyprotein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3
CC protease, involving isolating the protease in the presence of a
CC chaotropic agent, refolding the isolated protease by contacting it with a
CC chaotropic agent, and LDAO in the presence of reduced concentration of the
CC chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3
CC protease, involving diluting refolded inactive NS2/3 protease in a medium
CC containing an activation detergent to induce auto-cleavage of the NS2/3
CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3
CC protease, involving incubating the active NS2/3 protease and produce
CC cleavage products or their fragments, and measuring the presence or
CC absence of uncleaved NS2/3 protease, and measuring the presence or
CC absence of uncleaved NS2/3 protease, cleavage products or their fragments
CC and (6) screening a potential inhibitor of auto-cleavage activity of an
CC active NS2/3 protease, involving carrying out M3 in the presence of, or
CC absence of the potential inhibitor, comparing the amount of uncleaved
CC NS2/3 protease, cleavage products or their fragments. The protease is
CC useful for detailed biochemical characterisation of the enzymes and in
CC cute disease, which are useful as therapeutic agents against HCV
CC infection (which causes chronic liver disease, cirrhosis and end-stage
CC liver disease. M1 is useful for high level production of protease. The
CC present sequence represents the NS2/3 truncation mutant 827-1206
CC (numbered relative to the full length NS2/3 proteasin)
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361
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                                                                                                                                                                                    QSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCG
                                                                                                                                                                                                                                                              GREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTAT
                                                                                                                                                                                                                                                                                                                                             TYVYDHLTPLQDWAHAGİRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARR 193
                                                                                                                                                                                                                                                                                                                                                                                                    DITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTG
                                                                                                                                                                                                                                                                                                                                                                                                                                DITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACKLVRKAAGGHYVQMAFMKLAALTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALLTLSPYYKVLLARLIWMLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIF 73
                       RGVAKAVDFIPVESMETTMR
                                                                                                                SSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCT
                                                                                                                                                                                                                                       GREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTAT
                                                                                                                                                                                                                                                                                                                   TYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARR
RGVAKAVDFIPVESMETTMR
                                                                                                                                                        QSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCG
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ilarity 100.0%;
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380
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Matches 369
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18-SEP-1992;
04-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a partial Hepatitis C Virus (HCV) polyprotein from the non-structral region. Partial proteinase sequences (AAR82692-93) are contained within this sequence. The proteinase can be used as anti-HCV agents. They can also be used to screen cpds. for their abblity to inhibit their proteolytic activity. In this way proteinase inhibitors can be identified. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-287962/38.
N-PSDB; AAT03960.
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An HCV proteinase active substance - which has activity as an agent and can be used to screen for proteinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAEN/)
(SUMQ )
(SOYA-)
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SUMITOMO METAL IND LTD.
SOYAKU GIJUTSU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                         MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
                                                                                                                                                                                                                                                                                                                                                                                          3010
                                                                                             QVDGEVQVLSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWPA
                                                                                                                                                                                                         VQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC 180
                                                                                                                                                                                                                                                                                            MAASCGGAVFVGLVLLTLSPYYKVFLARLIWWLQYFITRAEAHLQVWVPPLNVRGGRDAI
                     GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR
                                                                PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
                                                                                                          GDIISGLPVSARRGKEILLGPADSFGEQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                               GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                                                                                         ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVFYFVRAQGLIRACMLVRKAAGGHY
GHVVGIFRAAVCTRGVAKAVDFIFVESMETTMR
                                              PPGARSMTPCTCGSSDLYLVTRHADVVPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPS
                                                                                                                                                                                              VQMAFMKLAALTGTYVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKLITWGADTAAC
                                                                                                                                                                                                                                           ILLTCAVHPELIFDITKLLLAILGPLMVLQAGITRVPYFVRAQGLIRACMLVRKVAGGHY
                                                                                                                                                                                                                                                                                                                                        95.8%;
ilarity 93.9%;
Conservative 1
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92JP-00249240.
92JP-00325303.
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/note= "partial
992. .1907
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992. .1
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                         Score 1967; Di
Pred. No. 3.1e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteinase;
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3.1e-181;
hes 11;
1206
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                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT

360

300 1053 993 180 933 120 873 60

0

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AAR68622 standard; protein; 3010 AA.

XX

AC AAR68622;

XX

AC AAR68622;

XX

DT 16-OCT-2003 (revised)
DT 16-CCT-1995 (first entry)

XX

DE HCV protein cleavable with new serine;
DE HCV proteinase; serine; cleavage; hepatitis

XX

XX

Proteinase; serine; cleavage; hepatitis

XX

XX

Proteinase; serine; cleavage; hepatitis

XX

CS

Hepatitis C virus; Virus.

XX

XX

PR

Cleavage-site 2419..2420
FT

Cleavage-site 2419..2420
FT

Cleavage-site 2419..2420
FT

Cleavage-site 2419..2420
FT

Cleavage-site 2419..2420
FT

Cleavage-site 2419..2420
FT

CAMPY-1993; 93JP-00105666.

XX

PR

DF

O6-MAY-1993; 93JP-00105666.

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PR

O6-MAY-1993; 93JP-00105666.

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Best Local Similarity
Matches 368; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein from HCV (hepatitis C virus) (encoded by AAQ80498) is cleaved between amino acids 2419 and 2420, by a new serine protease, contg. the sequence of AAR68621. The proteinse is purified as a fused product with the dihydrofolate reductase protein by using a methotrexate column. It can be used for the development of an inhibitor for HCV proteinase. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New HCV-originated proteinase active substance - used for site-specific cleavage by an intermolecular reaction and the purification thereof.
                                                                                              1054
                                                                                                                                                     241
                                301
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                                                                                                                                     QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA
                                                                                                                                                                                                                                                                   GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAASCGGAVFVGLVLLTLSPYYKVFLARLIWWLQYFITRABAHLQVWVPPLNVRGGRDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGFLLCPS
                                                                                          QVDGEVQVLSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWPA
                                                                                                                                                                                                                  GDIISGLPVSARRGKEILLGPADSFGEQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                                                                                                                                                                                                                                  VQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
                                                                                                                                                                                                                                                                                                                                          VQMAFMKLAALTGTYVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKLITWGADTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILLTCAVHPELIFDITKLLLPILGPLMVLQAGITRVPYFVRAQGLIRACMLVRKVAGGHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 10-19; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cleavable with new serine proteinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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2419. .2420
/note= "Serine protease cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1962; DB 2;
Pred. No. 9.4e-181;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Š В

1114 361

PPGARSMTPCTCGSSDLYLVTRHADVVPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPS 1173

393

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RESULT 6
ADR68864
ADR68868
XXX ADR6886
XXX ADR6
XXX Hepa
XXX Hepa
XXX Hepa
XXX Hepa
XXX Hepa
XXX Hepa
XXX Hepa
XXX Hepa
XXX Regi
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Best Local S
Matches 368
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Synthetic.
                                                                                                                                                                                   Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                                                                                                                                                                                                                                         Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant #10.
                                                                                                                                                                                                                                                                                                                    ABG30601;
                                                                                                                                                                                                                                                                                                                                                          ABG30601 standard; protein;
                                     Misc-difference
                                                                         Misc-difference 882
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virus

2183 /note= "Wild type Met

substituted by

Location/Qualifiers abel= Arg, Lys

(first entry)

2201

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AAQ81559 encodes AAR68864 hepatitis C virus (HCV) RNA helicase. The DNA was used in the construction of an expression vector, which was used to transform a baculovirus host. The transformed baculovirus could then be used for the recombinant prodn. of HCV RNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of hepatitis C virus helicase gene in baculovirus - useful for large scale prodn. of RNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3010 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1-4; 9pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                        tch 95.5%;
al Similarity 93.6%;
368; Conservative 13
                                                                                                                                                                                          VQMAFMKLAALTGTYVYDHLTBLQDWAHAGLRDLAVAVBPVIFSDMEVKIITWGADTAAC 180
                                                                                                                                                                                                                                                                                                                             ILLTCAVHPELIFDITKLLLAILGPLMVLQAGITRVPYFVRAQGLIRACMLVRKVAGGHY
                                                                                                                                                                                                                                                                                                                                             ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY
                    GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
                                                                                 PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
                                                                                                                               QVDGEVQVLSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKAPITQMYTNVDQDLVGWPA
                                                                                                                                               QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA
                                                                                                                                                                                                                                                             VQMAFMKLAALTGTYVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKLITWGADTAAC
GHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR
                                                               PPGARSMTPCTCGSSDLYLVTRHADVVPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPS
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Pred. No. 1.2e-180;
13; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a self-replicating hepatitis C virus (HCV) coplynucleotide molecule comprising a 5'-non translated region (NTR), where guanine at position 1 is substituted for adenine, a HCV polyprotein cregion coding for a HCV polyprotein; and a 3'-NUR region. The self-creplicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating potential inhibitors of HCV replication. The HCV RNA molecule is also useful for efficiently establishing cell culture replication. The self-creplication is substituted for A, and therefore provides an alternative to position 1 is substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the CG (2042) C/R mutations, transduces and/or replicates with greater cefficiency. This amino acid sequence represents a mutant of the hepatitis C virus replicon APGK12 and contains the viral protease NS2/3, protease complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note: This sequence snown in ABG30580 using information given in the claims of the invention
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Best Local
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                       GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
                                                                                                                                                                                                                                      GDIISGLPVSARRGREILIGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN 240
                                                                                      PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
                                                                                                                                    QVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA
                                                                                                                                                             QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA
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                                                                   PPGARSLTPCTCGSSDLYLVTRHADVTPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
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Pred. No. 7.1e-180;
.4; Mismatches 13;
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61 ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY

120 64

MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI MAASCGGAVFVGLILLTLSPHYKLFLARLIWWLQYFITRAEAHLQVWIPPLNVRGGRDAV

Matches

366;

Conservative

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Indels

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Gaps

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Similarity

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RESULT 8
ABG30519
ID ABG3051
XX ABG3
XX ABG3
XX Z1-0
DT 21-0
DT 21-0
XX Self
KW Self
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XX Key
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                                                                                  The invention describes a self-replicating hepatitis C virus (HCV) colymucleotide molecule comprising a 5'-non translated region (NTR), combine at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein; and a 3'-NTR region. The self-creplicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating comprising a fell culture replication. The self-creplicating highlitors of HCV replication. The HCV RNA molecule is also useful for efficiently establishing cell culture replication. The self-creplicating polynucleotide molecule contains a 5'-NTR, where G at position 1 is substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the G[2042]C/R mutations, transduces and/or replicates with greater complex NSJ/4, helicase NSJ and RNA-dependent RNA polymerase NSJB. Note: C virus replicate NSJ and RNA-dependent RNA polymerase NSSB. Note: C complex NSJ/4, helicase NSJ and RNA-dependent RNA polymerase NSDB. Note: C with sequence does not appear in the specification but has been created complex NSJ/4, helicase NSJ and RNA-dependent RNA polymerase NSSB. Note: C with the wild type sequence shown in ABGJ0580 using information given in the claims of the invention
                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New self-replicating RNA molecules from Hepatitis C virus (HCV), which possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
                                                                               Sequence 2201 AA;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-575382/61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Ser substituted by Gly" 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Arg, Lys
                   95.0%;
Score 1951; DB 5;
Pred. No. 7.1e-180;
.4; Mismatches 13;
                                       Length 2201;
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RESULT 9
ABG30600
ID ABG30600
ID ABG3
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The invention describes a self-replicating hepatitis C virus (HCV) polynucleotide molecule comprising a 5'-non translated region (NTR), where guanthe at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein; and a 3'-NTR region. The self-replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating potential inhibitors of HCV replication. The HCV RNA molecule is also useful for efficiently establishing cell culture replication. The self-
                                                                                                                                                                                                                                                                     New self-replicating RNA molecules from Hepatitis C virus (HCV), possess enhanced transduction or replication efficiency, useful i evaluating potential inhibitors of HCV replication.
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                                                                                                                                                                                                                    3; Page; 140pp; English
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1357
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RESULT 10
ABG30581
ID ABG30581
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  Kukolj G,
                                                                                                                                                                                                                                                                                                                                                                                  Self-replicating; hepatitis C virus; cell culture replication; NS2/3; NS3
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                                                                                                         22-DEC-2000; 2000US-0257857P
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14; Mismatches 13;
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Best Local Sim:
Matches 366;
  Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                                                          Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant #4.
                                                                                                                                         ABG30593
                                                                                                                                                                            ABG30593 standard; protein; 2201
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N-PSDB; ABK88573.
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Pred. No. 7.1e-180;
A; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                   The invention describes a self-replicating hepatitis C virus (HCV) coplynucleotide molecule comprising a 5'-non translated region (NTR), CC where guanine at position 1 is substituted for adenine, a HCV polyprotein core region coding for a HCV polyprotein; and a 3'-NTR region. The self-crepicating Hepatitis C virus (HCV) RNA molecule is useful for exclicitantly establishing cell culture replication. The self-creplicating polynucleotide molecule contains a 5'-NTR, where G at complex into substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the CG (2042) C/R mutations, transduces and/or replicates with greater CC efficiency. This amino acid sequence represente a mutant of the hepatitis complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS2B. Note: Chis sequence does not appear in the specification but has been created cc the claims of the invention
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New self-replicating RNA molecules from Hepatitis C virus (HCV), which possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
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                                                                                                                                                                                                                                                        1 MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
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QVEGEVQVVSTATQSFLATCVNGVCWTVEHGAGSKTLAGPKGF1TQMYTNVDQDLVGWQA
                                                                                                                                                                                            ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY
                                                                    GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                  VQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
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                                                GDIILGLPVSARRGREIHLGPADSLEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDRN
                                                                                                                                                                        MAASCGGAVFVGLILLTLSPHYKLFLARLIWWLQYFITRAEAHLQVWIPPLNVRGGRDAV
                                                                                                              VQMALMKLAALTGTYVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKVITWGADTAAC
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                                              The invention describes a self-replicating hepatitis C virus (HCV)
polynucleotide molecule comprising a 5'-non translated region (NTR),
compared planning at position 1 is substituted for adenine, a HCV polyprotein coronic coding for a HCV polyprotein, and a 3'-NTR region. The self-
comprising Hepatitis C virus (HCV) RNA molecule is useful for evaluating potential inhibitors of HCV replication. The HCV RNA molecule is also cuseful for efficiently establishing cell culture replication. The self-
complicating polynucleotide molecule contains a 5'-NTR, where G at comprisition is substituted for A, and therefore provides an alternative to constiting systems comprising a self-replicating HCV RNA molecule that, in conjunction with mutations in the HCV non-structural region, such as the CG (2042)C/R mutations, transduces and/or replicates with greater complexities and contains the viral protease NS21, protease complex consisting the viral protease NS21, protease complex consistency. This amino acid sequence is encoded by the hepatitis C virus consistency and RNA-dependent RNA polymerase NS5B Note: this consistency was presented from replicon APGK12 shown in ABG30581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New self-replicating RNA molecules from Hepatitis C virus (HCV), who possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 59-69; 140pp; English.
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Query Match

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Length 2201;

The invention describes a self-replicating hepatitis C virus (HCV) polynucleotide molecule comprising a 5'-non translated region (NTR)

Sequence

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                                                            New self-replicating RNA molecules from Hepatitis C virus (HCV), which possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
                                                                                                                                                                                                                                                                                                                                                            Self-replicating; hepatitis C virus; HCV; HCV replication cell culture replication; NS2/3; NS3/4; NS3; NS5B.
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                                      Disclosure; Page 69-74; 140pp; English
                                                                                                              WPI; 2002-575382/61
                                                                                                                                      Kukolj G,
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                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
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                                                                                                                      20-DEC-2001; 2001WO-CA001843
                                                                                                                                                                                   04-JUL-2002
                                                                                                                                                                                                                                                WO200252015-A2
                                                                                                                                                                                                                                                                                                         Hepatitis C virus
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                                                                22-DEC-2000; 2000US-0257857P
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14; Mismatches 13;
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N-PSDB; ABK88587.
              Hepatitis C virus NS2/3, NS3/4,
                                                 21-OCT-2002
                                                                                                                     ABG30599 standard; protein; 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2201 AA;
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                                                                                                                                                                                                                                                                                              PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGFLLCPS
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Pred. No. 7.1e-180;
.4; Mismatches 13;
                    NS3
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                  and NS5B mutant #8
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The invention describes a self-replicating hepatitis C virus (HCV) polymucleotide molecule comprising a 5'-non translated region (NTR), where guanine at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein, and a 3'-NTR region. The self-replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating potential inhibitors of HCV replication. The HCV RNA molecule is also useful for efficiently establishing cell culture replication. The self-replication is substituted for A, and therefore provides an alternative to position 1 is substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the G(2042) C/R mutations, transduces and/or replicates with greater efficiency. This amino acid sequence represents a mutant of the hepatitis C virus replicase NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS2/3, protease complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note: This sequence shown in ABG30580 using information given in the claims of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page; 140pp; English
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Synthetic.
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GDIILGLÞVSARRGREIHLGPADSLEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDRN 244
                                                           GDIISGLEVSARRGREILLGEADNFEGOGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN 240
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                                                                                                                                 VQMALMKLAALTGTYVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKVITWGADTAAC
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														oligopeptide abc	

ALIGNMENTS

genome polyprotein - hepatitis C virus (strain J)
N;Contains; capsid protein C; envelope protein M; major envelope protein E; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 19-Jan-2001
C;Accession: A39253; PS0086

R;Kato, N.; Hijikata, M.; Cotsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
A;Title: Molecular cloning of the human hepatitis C virus genome from Japanese A;Reference number: A39253, MUID:91088550; PMID:2175903
A;Recession: A39253

from Japanese patients v

T.; Shimoto

probable transport A;Molecule type: genomic RNA
A;Residues: 2650-2707 <kR2>
A;Residues: 2650-2707 typanese isolate
A;Reparimental source: Japanese isolate
C;Comment: The cleavage sites of this polyprotein have not been determined.
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serine
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-19/Product: envelope protein N #status predicted <VEE>
F;390-729/Product: major envelope protein E #status predicted <NS1>
F;300-729/Product: nonstructural protein NS1 #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1310-133/Region: nucleotide-binding motif A (P-loop)
F;1316-3191/Region: nucleotide-binding motif A (P-loop)
F;1363-2013/Product: nonstructural protein NS4 #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS5 #status predicted <N4B>
F;1363-2013/Product: nonstructural protein NS5 #status predicted <N4B>
F;196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,2041,2077,2240,27 밁 A;Molecule type: genomic RNA
A;Residues: 1-3010 <RAT>
A;Residues: 1-3010 <RAT>
A;Cross-references: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
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A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611
A;Cross-verses: GB:D90208; NID:g221610; PIDN:G20208; PIDN:g221610; PID:g221610; PID:g2 Ś S A;Reference number: PS0085 A;Accession: PS0086 Matches Query Match Best Local (874 814 MAASCGGAVFVGLVLLTLSPYYKVFLARLIWWLQYFITRAEAHLQVWVPPLNVRGGRDAI 369; 1 MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI 60 Similarity 95.8%; Score 1967; DB 1; ilarity 93.9%; Pred. No. 1.8e-153; Conservative 13; Mismatches 11; Length 3010; Indels 0 Gaps 873

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                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIN:106206, NCBIP:106207)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein;
F;2-115_Product: capsid protein C #status predicted <CPC>
F;116-191_Product: envelope protein M #status predicted <CPC>
F;116-191_Product: major envelope protein E #status predicted <MEE>
F;192-389_Product: nonstructural protein NS1 #status predicted <MEE>
F;300-729_Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1015_Product: hepacivirin #status predicted <NS2>
F;1007-1015_Product: hepacivirin #status predicted <NS3>
F;1230-1237_Region: nucleotide-binding motif A (P-loop)
F;1312-1317_Region: nucleotide-binding motif B
F;1516-1319_Region: DEXH motif
F;1516-1319_Product: nonstructural protein NS4a #status predicted <N4B>
F;1616-3013_Product: nonstructural protein NS4a #status predicted <N4B>
F;1616-3013_Product: nonstructural protein NS5 #status predicted <N4B>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome polyprotein - hepatitis C virus (strain JT)
N,Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
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A;Experimental source: HCV-JT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3010 <TAN>
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                                                                        VQMAFMKLAALTGTYVYDHLTFLQDWAHAGLRDLAVAVEFVIFSDMEVKIITWGADTAAC 180
                                                                                                                                                                                                 MAASCGGVVFVGLILLTLSPHYKVFLARLIWWLQYFITRAEAHLCVWVPPLNVRGGRDAI
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93.6%;
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Pred. No. 4.7e-152;
9; Mismatches 16;
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genome polyprotein - hepatitis C virus (strain Taiwan)
N;Contains: capsid protein C; envelope protein M; hepacivirin (E)
protein NS4a; nonstructural protein NS4b; nonstructural protein
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QVEGEVQVVSTATQSFLATCINGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWHA
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                   QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGFITQMYTNVDQDLVGWQA
                                                                             GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
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                                                                                                                        VQMALMKLAALTGTYVYDHLTPLQDWAHTGLRDLAVAVBPVVFSDMETKIITWGADTAAC
                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                          94.3%;
                                                                                                                                                                                                                                                                                                           Score 1935; DB 1;
Pred. No. 8.1e-151;
7; Mismatches 15;
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A, McCessidue: 1937/07
A, McCessidue: 1937/07
A, Mesidues: 1-547, TT, 549-621, TV, 623-624, ST, 626-652, DL', 655-761, TT, 763-782 <hG>
A, Residues: 1-547, TT, 549-621, TV, 623-624, ST, 626-652, DL', 655-761, TT, 763-782 <hG>
A, Residues: 1-547, TT, 549-621, TV, 623-624, ST, 626-652, DL', 655-761, TT, 763-782 <hG>
A, Cross references: EMBL: X61991
A, Note: this sequence is inconsistent with the nucleotide translation
A, Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
as Trp, and TTC for residue 771 as Ser
A, Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 771 as Ser
A, Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 771 as Ser
A, Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 771 as Ser
A, Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 772 as Ser
A, Note: the authors translated the codon AGG for residue 4200
as Trp, and TTC for residue 771 as Ser
A, Note: the authors translated the codon AGG for residue 4200
as Trp, and TTC for residue 771 as Ser
A, Note: the authors translated the codon AGG for residue 4200
as Trp, and TTC for residue 771 as Ser
A, Note: the sequence extracted from NCBI backbone (NCBIN: 121747), NCBIP: 121748)
C, Superfamily: hepatitis C virus genome polyprotein
C, Keywords: ATP, 121748)
C, Superfamily: hepatitis C virus genome polyprotein
C, Keywords: ATP, 121748)
C, Superfamily: hepatitis C virus genome polyprotein
C, Keywords: ATP, 121748)
C, Superfamily: hepatitis C virus genome polyprotein
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C, Superfamily: hepatitis C virus genome polyprotein
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C, Superfamily: hepatitis C virus genome polyprotein
C, Keywords: ATP, 121748, NCBIP: 121747, NCBIP: 121748
C, Superfamily: hepatitis C virus genome polyprotein
C, Keywords: ATP, 121748
C, Superfamily: hepatitis C virus genome polyprotein
C, Keywords: ATP
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
A;Variety: isolate JK1
C;Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 23-Mar-2001
C;Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 23-Mar-2001
C;Accession: $18030, S3570; A83332; $18029
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Bescription: A whole genome of hepatitis C virus cDNA was isolated from a s:
A;Reference number: $18030
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A; Residues: 1-3010 < HCN>
A; Residues: 1-3010 < HCN>
A; Cross-references: EMBL:X61596; NID:g59478; PIDN:CAA43793.1; PID:g59479
A; Experimental source: isolate JK1 from an individual
R; Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A; Title: Sequence analysis of putative structural regions of hepatitis C virus isolated
A; Reference number: A48332; MUID:93119270; PMID:8380322
A; Accession: S33570
A; Accession: S33570
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                                 GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
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Pred. No. 9.3e-149;
.3; Mismatches 19;
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A;Residues: 1-3010 <TAX>
A;Residues: 1-3010 <TAX>
A;Residues: 1-3010 <TAX>
A;Cross-references: EMBL:M58335; NID:g329770; PIDN:AAA72945.1; PID:g329771
A;Cross-references: EMBL:M58335; NID:g329770; PiDN:AAA72945.1; PID:g329771
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nons
F;2-115/Product: capsid protein (# status predicted <CPC>
F;116-191/Product: major envelope protein E #status predicted <MEE>
F;192-389/Product: monstructural protein NS1 #status predicted <NS1>
F;390-729/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1312-3137/Region: nucleotide-binding motif A (P-loop)
F;3112-3137/Region: nucleotide-binding motif B
F;1316-1319/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1616-3010/Product: nonstructural protein NS5 #status predicted <N4A>
F;1616-3010/Product: nonstructural protein NS5 #status predicted <N4S5
F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041
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PPGARSMTPCTCGSSDLYLVTRHADVI PVRRRGDSRGSLLSPRPVSYLKGSSGGFLLCPS
                                                                                                                                            QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGFKGFITQMYTNVDQDLVGWQA 300
                                                                                                QVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAAPKGPITQMYTNVDQDLVGWPK 1113
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A;Reference number: A38465; MUID:91140698; A;Accession: A38465
                                                                                                                              C/Species: hepatitis C virus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Jan-2001
C/Accession: A38465
                                                                                  R;Takamizawa, A.; Mori, C.; Fuke, J. Virol. 65, 1105-1113, 1991
                                                                                                                                                                                                                        genome polyprotein - hepatitis C virus N;Contains: capsid protein C; envelope protein
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                                                                                                                                                                                                     nonstructural protein
                                                                                                           I.; Manabe,
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                                         hepatitis C virus PMID:1847440
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GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN | VQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC 180 ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY 120 MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI 60 VQMAFMKLGALTGTYIYNHLTPLRDWPRAGLRDLAVAVEPVVFSDMETKIITWGADTAAC ILLMCAVHPELIFDITKLLIAILGPLMVLQAGITRVPYFVRAQGLIHACMLVRKVAGGHY 92.0%; Score 1888; DB 1; 90.8%; Pred. No. 6.1e-147; tive 13; Mismatches 23; Length 3010; Indels ted <NS5>,645,1213,1255,2041,2077,224 0; 873 240 993 933

В

1114

PPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPF

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A;Molecule type: mRNA
A;Residues: 1-3011 <CHO>
A;Residues: 1-3011 <CHO>
A;Cross-references: GB:M62321; NID:g329873; PIDN:AAA45676.1; PID:g329874
A;Chan, S.W.; McCmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new heatitis C virus type and its phylogenetic relationship A;Reference number: PQ0393; MUID:92268871; PMID:1316939
A;Accession: PQ0403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 19-Jan-2001 C;Accession: A39166; PQ0403; PQ0404 R;Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Galle Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991 A;Title: Genetic organization and diversity of the hepatitis C virus. A;Reference number: A39166; MUID:91172826; PMID:1848704
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A;Residues: 1577-1633 <CHA>
A;Cross-references: DDBJ:D10128
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NyContains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C/species: hepatitis C virus
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A,Nolecule type: genomic RNA
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: 1577-1633 <CH2>
A,Rosidues: chapsid protein; envelope protein; glycoprotein; hydrolase; nonstructural protein R; glycoprotein; hydrolase; nonstructural protein R; status predicted <CPC>
F; 116-191/Product: envelope protein R; status predicted <MEE>
F; 120-389/Product: nonstructural protein NS1 #status predicted <NS1>
F; 130-729/Product: nonstructural protein NS2 #status predicted <NS2>
F; 130-1006/Product: hepacivirin #status predicted <NS3>
F; 130-1317/Region: nucleotide-binding motif A (P-loop)
F; 1316-1319/Region: bEXH motif B
F; 1316-1319/Region: bEXH motif B
F; 1316-1319/Region: bEXH motif B
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                                                       GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                                           ILLMCAVHPTLVFDITKLLLAVFGPLWILQASLLKVPYFVRVQGLLRFCALARKMIGGHY
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                    GDIINGLPVSARRGREILLGPADGMVSKGWRLLAPITAYAQQTRGLLGCIITSLTGRDKN
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genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C;Accession: S40770; PC1285
R;Okamoto, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S40770
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Best Local Similarity
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                                                                                                                                                                                               814 VAASCGGVVLVGLMALTLSPYYKRCISWCLMWLQYFLTRVBAQLHVWVPPLNVRGGRDAV
                                                                                                                                                                                                                                                          320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OVEGEVOIVSTAAOTFLATCINGVCWTVYHGAGTRTIASFKGPVIOMYTNVDQDLVGWPA
                                                                                                  VQMAFMKLAALTGTYVVDHLTBLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
                                                                                                                                        GHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR
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                                                                                   VQMAIIKLGALTGTYVYNHLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLITWGADTAAC
                                                                                                                                                                                                                  MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA
                                             GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN 240
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                     85.6%;
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                                                                                                                                                                                                                                                                       Score 1758; DB 1; Pred. No. 3.2e-136;
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                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                   Length 3011;
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A;Note: neither amino acid nor nucleotide sequence is given
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; dydrolase; nonstructura
F;1-115/Product: capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
F;1-115/Product: capsid protein C #status predicted <CPC>
F;192-389/Product: major envelope protein M #status predicted <MEB>
F;192-389/Product: nonstructural protein NS1 #status predicted <NS1>
F;390-729/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F;1130-1237/Region: nucleotide-binding motif A (P-loop)
F;312-1317/Region: DEXH motif
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N43>
F;1014-3011/Product: nonstructural protein NS4b #status predicted <NS5>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;1016-1862/Product: nonstructural protein NS6 #status predicted <NS5>
F;1016-1862/Product: nonstructural protein NS6 #status predicted <NS5>
F;1016-1862/Product: nonstructural protein NS6 #status predicted <NS5>
F;1016-1862/Product: nonstructural protein NS6 #status predicted <NS5>
F;1016-1862/Product: nonstructural protein NS6 #status predicted <NS5>
F;1016-1862/Product: nonstructural protein NS6 #status predicted <NS5>
F;1016-1862/Product: nonstructural protein NS6 #status predicted <NS5>
F;1016-1862/Production NS6 #status predicted <NS5>
F;1016-1862/Production NS6 #status predicted <NS6-1862/P
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A;Residues: 1-3011 < INC>
A;Residues: 1-3011 < INC>
A;Residues: 1-3011 < INC>
A;Cross-references: GB.M67463; NID:g329737; PIDN:AAA45534.1; PID:g329738
A;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A;Title: Genomic structure of the human prototype strain H of hepatitis C virus:
A;Reference number: A41546; MUID:92052256; PMID:1658800
A;Contents: annotation
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 19-Jan-2001
C;Accession: A36814, A41546
R;Inchauspe, G:; Zebedee, S:; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
submitted to GenBank, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: Genomic structure A;Reference number: A36814 A;Accession: A36814
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Local Similarity 81.4%; Pred. No. 1e-135;
hes 320; Conservative 36; Mismatches 37; Indels 0
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QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGFKGPITQMYTNVDQDLVGWQA
                                                                                                                                   GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
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                                                                                            VQMAIIKLGALTGTCVYNHLAPLRDWAHNGLRDLAVAVEPVVFSRMETKLITWGADTAAC
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VQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYINVDQDLVGWQAPPGAR

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GLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGE

245

VLPVSARRGREIFLGPADDIKTSGWRLLAPITAYAQQTRGVLGAIVLSLTGRDKNEAEGE

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R;Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M. Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A;Title: The complete coding sequence of hepatitis C virus genotype 5a, the partitle: The complete coding sequence of hepatitis C virus genotype 5a, the partitle: The complete coding sequence of hepatitis C virus genotype 5a, A;Title: The complete in T.C5620
A;Accession: JC5620
A;Accession: JC5620
A;Accession: JC5620; MUID:97366593; PMID:923423
A;Accession: JC5620
A;Molecule type: mRNA
A;Residues: 1-3014 < CHA>
A;Cross-references: GB:Y13184
A;Cross-references: GB:Y13184
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C;Accession: JC5620
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 267; Conserv
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GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
|||||:|||||||||||||::|||||
GHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 1206
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                                                                                                                                                                       Conservative
                                                                                                                                                                                                             72.7%;
                                                                                                                                                                       56;
                                                                                                                                                                  Score 1493; DB 1;
Pred. No. 2.3e-114;
6; Mismatches 65;
                                                                                                                                                                                                                                                    Length 3014;
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A;Molecule type: genomic RNA
A;Residues: 1-303 cOXA>
A;Residues: 1-303 cOXA>
A;Cross-references: GB:D00944; NID:g221650; PIDN:BAA00792.1; PID:g221651
A;Cross-references: GB:D00944; NID:g221650; A;Cross-references: GB:D00944; NID:g221650; A;Cross-references: GB:D00944; NID:g221650; A;Cross-references: GB:D00944; NID:g221650; A;Cross-references: GB:D00944; NID:g221650; A;Cross-references: GB:D00946; A; RESULT 11 GNWVJ8 8 밁 á Ś 吊 밁 맑 Ś 밁 Ś В Š 뭐 S R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H. J. Gen. Virol. 72, 2697-2704, 1991
A;Title: Nucleotide sequence of the genomic RNA of hepatitis A;Reference number: JQ1303; MUID:92044440; PMID:1658196
A;Accession: JQ1303 genome polyprotein - hepatitis C virus (isolate HC-J6) N;Contains: capsid protein C; envelope protein M; hepaciv protein NS4a; nonstructural protein NS4b; nonstructural C;Species: hepatitis C virus 밁 Ş Query Ma Best Loc Matches Date: 19-May-2000 #sequence_revision Accession: JQ1303 Match 1123 1063 1003 1180 1183 366 306 246 186 943 883 823 252; 366 6 Similarity MKLAALIGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIIS AVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAF GLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGE LALGRWTGTYIYDHLTPMSDWAANGLRDLAVAVEPIIFSPMEKKVIVWGAETAACGDILH IFRAAVCTRGVAKAVDFIPVESMETTMR SLEPCI SMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVG IQVLSTVTQSFLGTTISGVLWTVYHGAGNKTLAGSRGPVTQMYSSAEGDLVGWPSPPGTK 1122 VQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGAR GLPVSARLGREVLLGPADGYTSKGWSLLAPITAYAQQTRGLLGTIVVSMTGRDKTEQAGE GAALLVLITLFTLTPGYKTLLSRFLWWLCYLLTLABAMVQBWAPPMQVRGGRDGIIWAVA GGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTC IFRAAVCTRGVAKAVDFIPVESMETTMR Conservative 64.9%; 58; Pred. No. 6.2e-107; Mismatches 19-May-2000 393 393 M; hepacivirin #text_change 17-Nov-2000 Length 3033; Indels protein Ή. a (EC virus Machida, 0 C 3.4.21.98) NS5 isolated from A.; Miyakawa, 1002 305 1062 1182 365 185 245 942 125 882 9 (nonstruct) Ω. hun

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A;Molecule type: genomic RNA
A;Residues: 1-3033 cOXA>
A;Cross-references: GB:D10988; GB:D01221; NID:g221608; PIDN:BAA01761.1; PID:g221609
A;Cross-references: GB:D10988; GB:D01221; NID:g221608; PIDN:BAA01761.1; PID:g221609
A;Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L.
J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to experience number: PQ0393; MUID:g2288871; PMID:1318939
A;Reference number: PQ0397
A;Molecule type: genomic RNA
A;Residues: 2678-2754 <CHA>
A;Experimental source: isolate E-b12
R;Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno, Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A;Title: Distribution of plural HCV types in Japan.
A;Reference number: PQ0554; MUID:g2068204; PMID:1720309
A;Accession: PQ0554; MUID:g2068204; PMID:1720309
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F;1867-2011/Product: nonstructural protein NS4b #status predicted <N4B>
F;2018-3033/Product: nonstructural protein NS5 #status predicted <N85>
F;196,209,233,299,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,23:
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A; Residues: 2678-2729 < KAT>
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A;Title: Full-length sequence of a hepatitis C virus genome A;Reference number: A40250; MUID:92230232; PMID:1314459
A;Accession: A40250
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
C;Accession: A40250; PQ0397; PQ0559
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SMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVG
                                                                                                   VQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGAR
                                                                                                                                                             GLPVSARLGREVILGPADGYTSKGWKLLAPITAYTQQTRGLLGAIVVSLTGRDKNEQAGQ
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                                                                                                                                                                                                                                                                                                                                             ILHPRIVFEVTKWILAILGPAYLIKASIIRIPYFVRAHALIRVCTIVKHIAGARYIQMIL
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Pred. No. 9e-107;
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M; hepacivirin (EC 3.4.21.98)
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C;Coesion: T08841
R;Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.; Mushahwar, I
J. Gen. Virol. 79, 41-45, 1998
A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.
A;Reference number: Z16486; MUID:98120818; PMID:9460920
A;Reference number: Z16486; MUID:98120818; PMID:9460920
A;Rocession: T08841
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3005 <ERK>
A;Cross-references: EMBL:AFF023425; NID:92828599; PIDN:AAC40502.1; PID:92828600
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                       polyprotein - marmoset hepatitis GB virus A
C;Species: marmoset hepatitis GB virus A
C;Species: marmoset hepatitis GB virus A
C;Species: marmoset hepatitis GB virus A
C;Accession: T08839
R;Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.; Mushahwar, I.K.
J. Gen. Virol. 79, 41-45, 1998
A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.
A;Reference number: Z16486; MUID:98120818; pMID:9460920
A;Accession: T08839
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: genomic RNA
A;Residues: 1-2970 CERK>
A;Rooss-references: EMBL/RF023424; NID:92828597; PIDN:AAC40501.1; PID:92828598
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
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Similarity 31.3%; Pred. No. 6.5e-25;
11; Conservative 57; Mismatches 154;
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                                          227
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                                                                                                                       189
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                                                                                                                                                                                                  132 LCML---FSKKPFAVFLESAGYTHEDVLLQKPKAGVGHIMQPAFTIIRDTNSKCILLLIR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                     26 LARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIFDITKLLLAIFGP
                                                                                                                                                                                                                                                                                83 IADLAFGINYLMRR-----QGNFPTASVYAGSNCIEL----KGPEIIMDLTELLR--FLT
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                           -----KLAALTGTYVYDHLTELQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAA 179
  DKNQVEGEVQVVSTA---
                                                                              CGDIISGLEVSARRGREILLGPADNFEGQGW--RLLAPITAYSQQTRGLLGCIITSLTGR
                                                                                                                       GTHSIKDTLTAATGAVVPFHHSVLHD--
                                                                                                                                                                                                                                          LMVLQAGITKVPY--FVRAQGLIRACMLVR--KAAGGHYVQMAFM------
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Query

Match

16 . 78;

Score

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Length

-TQSFLATCV---

--NGVCWTVFHGAGSKTLAGPKGP--I

284 248 237

WIAKLSVP-

CLLKAL---

-GGLSNLVLGY--

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226

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130 ALTGTYVYDHLTPLQD--WAHAG-----LRDLAVAVEPVIFSDMEVKIITWGADTA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      816 LVAAWFWPREIAAVCVAFILGFGFFDVVDYILEVVLVSSPNLVRLARVLDSLVAAGDKLA
                                                                                                                                                                                                                                                                                  SLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVD 292
                                                                                                                                                                                                                                                                                                                                               SCGQSVHGKPVVARRGDEVLIGVLNGV----WELPPGFVPTAPVVVH-HHGKGFFGVVKT
                                                                                                                                                                                                                                                                                                                                                                                                          ACGDIISGLPVSARRGREILLGPADNFEGQGWRL-----LAPITAYSQQTRGLLGCIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T---TWLVEKLRKRNCFLYAHAGQVTRRTAEQLRQWGFALEPVAVHPEDCAMVRDAARTL 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLAIFGP-----LMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLA
PAELCDFRGSSGSPILCDEGHAVGML-ISVLHRGSRVTGIRYTKPWETLPREAITHT 1150
                                                 PRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRG-----VAKAVDFIPVESMETT
                                                                                                                 DDVAVYPLPVGAKCLEPCKCQPQGVWVI-
                                                                                                                                                                      QDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLS------ 341
                                                                                                                                                                                                                                SMTGWDETEHVGNVVVLGTSTTRSMGTCVNGVMYTTYHGSNARTLAAQMGPVNSRWWSAS 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56
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6; Mismatches 133;
                                                                                                                        -RND-
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                                                                                                                     -GALCHGTLGRTVELDL 1094
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                                                                                                                                                                                                                                                                                                                                                           987
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A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Anso C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal: A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-692 <BEV> A;Cross-references: GB:Z97340; NID:g2244950; PID:e327492; PID:g2244965 C;Genetics: A;Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Punk, Nature 391, 485-488, 1998
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Score 112; DB Pred. No. 0.3; 45; Mismatches

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Length 692;

135; 2

Indels

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Gaps

23;

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earch	B 성	40 40	Db Qy	dd Qy	å S	B 8	B &	Query Ma Best Loc Matches	Db 36 RESULT 15 VHWWH2 Structural p. C;Species: 30-S. C;Date: 30-S. C;Accession: R;Tan, A.W.; Yirology 185 A;Tele: Hep. A;Reference:	Фр	Db
completed: May 6, 2004, 09:37:17	342 PRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPV 385	286 QMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRG-SILS 341	258 ATCVNGVCWTVFHGAGSKTLAGPKG-PIT 285	237 257 237	185 SGLPVSARRGREILLGPADNFEGOGWRLLAPI-TAYSQQTRGLLGCIITSLTG 236 :	125 FMKLAALTGTYVYDHLTPLODWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDII 184 	76 TKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMA 124	ry Match 5.0%; Score 102.5; DB 1; Length 660; Local Similarity 19.8%; Pred. No. 1.7; Ches 82; Conservative 52; Mismatches 130; Indels 151; Gaps 19;	Qy 341 SPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVD 381	285 TQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIP-VRRRGDSRGSLL 340	: : : : ; ; ; ; ; ; ; ; ; ; ;

Search completed: May 6, 2004, 09:37:17 Job time: 14.7992 secs

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Result
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Maximum DB seq length: 200000000
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS	OPPC_BACSU	PTPV_MOUSE	NHAC_BACSU	CLR3_RAT	PWP2_SCHPO	HELS_METMA	NRAM_IATRA	YP71_MYCTU	RIR1_HSVEB	DCUA_WOLSU	GALE_NEIGO .	NRAM_IAWHM
	P24139 bacillus su			088278 rattus norv			P03472 influenza a	Q50650 mycobacteri				

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	an email to license@isb-sib.ch).	remitres a license agreement (See http://www.isb-sib.ch/annour	-profit institutions as long as its cont	bean Bioinformatics Institute. There are no restrictions on	een the Swiss Institute of Bioinformatics and the EMBL outstation	is SWISS-PROT entry is copyright. It is produced throug		I SIMILARITY: THE PROTEASE BELONGS	and mony	x= The micleocapsid is a complex	The envelope Consists of	מל ליינים	• •	Cys or Thr in Pl and Ser or Ala in Pl'.	precursor polyprotein, commonly with Asp or Glu in the P6	գե	in the wirel BNA replication.	e small pro	280:325-328(1991).	ß :	, 000001 41114 411 1144	TIPALEO; PUDMECHICAPAGO;	-		Sci. U.S.A.	n-B hepatitis.";	ocommo k.; of the human hepatitis	Kato N., Hljikata M., Cotsuyama Y., Nakagawa M., OHKOSHI S.,	Med=2175903;	•	- 1	NCHI TAXXID=11116:	Viruses; ssknA positive-strand viruses, no bus a raye; riavivititude,	s C virus (isolate Japanese) (HCV).	(P66) (P70) (RNA-dir	(P56); Nonstructural protein	3.4.22); Frocease/Herroase NSS (F70) (Repactivities)	68) (GP70) (NSI); Protein P7; Nonstructural protein NSZ (F	ope glycoprotein E1 (GP32) (GP35); Envelope glycoprot	enome polyprotein [Contains: Capsid protein C (Core protein)	003 (Rel. 41,	1992 (Rel. 2	52;	IT 1 POUJA STANDARD: PRT: 3010 AA	

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EMBL; D90208; BAA14233.1; -.

GNWVCJ

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Query Match
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InterPro; IPRO02519; HCV env.
InterPro; IPRO02518; HCV_NS1.
InterPro; IPRO02518; HCV_NS2.
InterPro; IPRO00745; HCV_NS4a.
InterPro; IPRO00745; HCV_NS4a.
InterPro; IPRO001400; HCV_NS5a.
InterPro; IPRO001650; HCV_RdRP.
InterPro; IPRO001650; HCV_RdRP.
InterPro; IPRO001650; HCV_RdRP.
InterPro; IPRO007094; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; RNA_Dol_DS_PS.
InterPro; IPRO07095; NNA_Dol_DS_PS.
InterPro; IPRO07095; NNA_Dol_DS_PS.
InterPro; IPRO07095; NNA_Dol_DS_PS.
InterPro; IPRO07095; NNA_Dol_DS_PS.
InterPro; IPRO07095; INTERPRO; I.
Pfam; PF01530; HCV_NS3; I.
Pfam; PF01530; HCV_NS4b; I.
Pfam; PF01006; HCV_NS4b; I.
Pfam; PF01006; HCV_NS4b; I.
Pfam; PF01006; HCV_NS4b; I.
Pfam; PF01007; Nn-Licase_C; I.
Pfam; PF00990; Viral_RdRP; I.
SMART; SM00487; DEMOC; I.
SMART; SM00487; DEMOC; I.
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REMOVED FROM CARSID PROTEIN C BY THE CELLULAR AMINOPEPTIDASE.
                                                                                                                                                        CARBOHYD
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MEROPS; U39.001;
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HSSP; P26663;
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IPR001410;
IPR002522;
                            LUXP.
                                                                           Cys_Ser_trypsin.
DEAD.
HCV_capsid.
HCV_core.
HCV_NS1.
HCV_NS1.
HCV_NS2.
HCV_NS4a.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
 95.8%;
                                                                                                                                                                                                                                                                   CAPSID PROTEIN C (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Gore protein E2 Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1; Protein P7; NOSTURCTURAL protein NS2 (GP58) (GP70); Nonstructural protein NS48 (P4); Nonstructural protein NS48 (P5); Nonstructural protein NS48 (P77); Nonstructural protein NS48 (P57); Nonstructural protein NS48 (P65) (F70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
NS5B (P66) (F70; (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate HC-JT) (HCV).
Hepacititis Systam positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                SEQUENCE FROM N.A.

MEDLINE=92295714; PubMed=1318627;

Tanaka T., Kato N., Nakagawa M., Ootsuyama Y., Cho M.J.,

Nakazawa T., Hijikata M., Ishimura Y., Shimotohno K.;

"Molecular cloning of hepatitis C virus genome from a single Japa carrier: sequence variation within the same individual and among infected individuals.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLG_HC
Q00269;
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=31642;
                                                                                                                                                                                                                                                                                                                                                                                                Hepacivirus.
          SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.

SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPGARSMTPCTCGSSDLYLVTRHADVVPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS 360
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3; Mismatches 11;
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MEROPS; S29,001; -.

MEROPS; U39,001; -.

MEROPS; U39,001; -.

InterPro; IPR003003; Cys Ser_trypsin.

InterPro; IPR001410; DEAD.

InterPro; IPR002521; HCV_capsid.

InterPro; IPR002521; HCV_capsid.

InterPro; IPR002521; HCV_NS1.

InterPro; IPR002518; HCV_NS2.

InterPro; IPR002518; HCV_NS4b.

InterPro; IPR0002566; HCV_NS4b.

InterPro; IPR001450; HCV_NS4b.

InterPro; IPR001650; Hclicase_C.

InterPro; IPR0017095; RNA_pol_DS_PS.

InterPro; IPR007095; RNA_pol_DS_PS.

InterPro; IPR007095; RNA_pol_DS_PS.

InterPro; IPR007094; RNA_pol_DS_PS.

InterPro; IPR007094; RNA_pol_DS_PS.

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InterPro; IPR007094; RNA_pol_DS_PS.

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MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN NS1/E2 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

RNA_DIRECTED RNA POLYMERASE (POTENTIAL).
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GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR
                                   GDIILGLPVSARRGREILLGPADSIEGQGWRLLAPITAYAQQTRGLLGCIVTSLTGRDKN
                                                                                                                      GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                               VQMAFMKLAALTGTYYYDHLTPLQDWAHAGLRDLAVAVEPVVFSDMETKIITWGADTAAC
                                                                                                                                                       VQMAFMKLAALTGTYVVDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
                                                                                                                                                                                                                   MAASCGGVVFVGLILLTLSPHYKVFLARLIWMLQYFITRABAHLCVWVPPLNVRGGRDAI
                                                                                                                                                                                                                                 MAASCGGAVFIGLALLTISPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
                                                                       QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWHA
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Pred. No. 4.2e-150;
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ID POLG_HCVTW

AC P29846;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

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DE (GE6) (GP70) (NS1); Protein Sc (GP35); Envelope glycoprotein NS2 (P21)

DE (GE6) (GP70); Nonstructural protein NS3 (P70) (Hepacivirin)

DE (EC 3.4-21-98); Nonstructural protein NS4A (P4); Nonstructural protein

DE NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].

OS Hepatitis C virus (isolate Talwan) (HCV).

OS Hepativirus

OC Viruses; SERNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Viruses; SERNA Positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus

OC WORL TaxID=31645;

RN (LI) (TaxID=31645;

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R Pfam; PF01543; HCV_capsid; 1.

R Pfam; PF01543; HCV_car; 1.

R Pfam; PF01539; HCV_env; 1.

R Pfam; PF01539; HCV_NS1; 1.

R Pfam; PF01506; HCV_NS2; 1.

R Pfam; PF01006; HCV_NS4; 1.

R Pfam; PF01006; HCV_NS46; 1.

R Pfam; PF01006; HCV_NS5a; 1.

R Pfam; PF01007; Hclicase C; 1.

R Pfam; PF0197; Viral_RdRP; 1.

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PDB; 1NS3; 08-APR-98.
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PIR; A40244; GNWVTW.
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SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
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SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY 829.
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730
1007
1616
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2014
347
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191
383
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HCV_core.
HCV_NS1.
HCV_NS2.
HCV_NS4a.
HCV_NS4b.
HCV_NS4b.
HCV_Rdsp.
HCV_Rdsc.
HCV_Rdsc.
HCV_Rdsc.
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DEAD.
                                                                                                                                                                                                                                                                                        CELULIAS ANIANOS (POTENTIAL).
CORE PROTEIN (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN 8 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE/HELICASE NS3 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
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CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
ATP (POTENTIAI)
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N-LINKED
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CHARGE RELAY SYSTEM (BY SIMI
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           (POTENTIAL)
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Query Match
Best Local S
Matches 361
                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (G932) (G935); Envelope glycoprotein E2 (G968) (G970) (NS1); Protein P7; (N935); Envelope glycoprotein E2 (G968) (G970) (NS1); Protein P7; (N935) (P70) (Hepacivirin)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS4B (P27); (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate EX) (HCV).
Viruses, SSNA positive-strand viruses, no DNA stage; Flaviviridae;
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P26663;
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X MEDLINE-98227846; PubMed=9568891;

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Love R.A., Parge H.E., Wick
Moomaw E.W., Adachi T., Hos
"The crystal structure of h
trypsin-like fold and a str
Cell 87:331-342(1996).
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MEDLINE=91140698; PubMed=1847440;

Takamizawa A., Mori C., Fuke I., Manabe S., Murakami S., Fujita J.,

Onishi E., Andoh T., Yoshida I., Okayama H.;

"Structure and organization of the hepatitis C virus genome isolated from human carriers.";
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or send an email to license@isb-sib.ch).
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"Non-structural protein 3 of hepatitis C v.
phosphorylation mediated by cAMP-dependent
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MEDLINE=97015088; PubMed=8861916;
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J. Virol. 65:1105-1113(1991).
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InterPro; IPR001490; HCV_NS4b.
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InterPro; IPR002166; HCV_Rdsp.
InterPro; IPR007094; Psptidase C29.
InterPro; IPR007099; RNA_pol_pS_PS.
InterPro; IPR007099; RNA_pol_pSvir.
Pfam; PP01543; HCV_core; 1.
Pfam; PP01542; HCV_core; 1.
Pfam; PP01543; HCV_NS1; 1.
Pfam; PP01560; HCV_NS2; 1.
Pfam; PP01506; HCV_NS3; 1.
Pfam; PP01006; HCV_NS4a; 1.
Pfam; PP01006; HCV_NS4a; 1.
Pfam; PP01506; HCV_NS4b; 1.
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Pfam; PP01508; Viral RdRP; 1.
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Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
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CAPSID PROTEIN C (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN US1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN US2 (POTENTIAL).

NONSTRUCTURAL PROTEIN US2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN US4A (POTENTIAL).

NONSTRUCTURAL PROTEIN US4A (POTENTIAL).

NONSTRUCTURAL PROTEIN US4B (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
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DR InterPro; IPR000252; HCV_capsid.

DR InterPro; IPR00252; HCV_capsid.

DR InterPro; IPR002519; HCV_NS1.

DR InterPro; IPR002519; HCV_NS1.

DR InterPro; IPR002519; HCV_NS4.

DR InterPro; IPR002519; HCV_NS4.

DR InterPro; IPR002519; HCV_NS4.

DR InterPro; IPR001490; HCV_NS4.

DR InterPro; IPR001650; HelTcase C.9.

DR InterPro; IPR0017094; RNA_pol_DS_PS.

DR InterPro; IPR007094; RNA_pol_PSvir.

DR InterPro; IPR007094; RNA_pol_PSvir.

DR Pfam; PP01542; HCV_capsid; 1.

DR Pfam; PP01539; HCV_NS1; 1.

DR Pfam; PP01539; HCV_NS4; 1.

DR Pfam; PP01539; HCV_NS4; 1.

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DR Pfam; PP01539; HCV_NS4; 1.

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DR Pfam; PP01004; HCV_NS5; 1.

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Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,
Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,
Bradley D.W., Kuo G., Houghton M.;
"Genetic organization and diversity of the hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
-!- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are
hydrophobic, suggesting a possible membrane-related function
and NS5 may play a role in the viral RNA replication.
-!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the
                                                                                                                                                                                                                  Transmembrane; Nonstructural
3D-structure.
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PDB; 1A1V; 16-FEB-99
PDB; 1HEI; 25-NOV-98
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-!- CATALYTY: N nucleoside triphosphate = N diphosphate
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MEROPS; U39.001;
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SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.

SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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1HEI; 25-NOV-98.
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CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
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DT 10-OCT-2003 (Rel. 42, L.
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                                                                                                                                             QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGFKGPITQMYTNVDQDLVGWQA
                                                                                                                                                                        GDIISGLFVSARRGREILLGPADNFEGQGWRLLAFITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                             VQMVIIKLGALTGTYVYNHLTPLRDWAHNGLRDLAVAVEPVVFSQMETKLITWGADTAAC
                                                                                                                                                                                                     VQMAFMKLAALIGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
                                                                                                                                                                                                                                 ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY
                                                                                                                                                                                                                                                     VAASCGGVVLVGLMALTLSPYYKRYISWCLWWLQYFLTRVEAQLHVWIPPLNVRGGRDAV
                                                                                                                                                                 GDIINGLPVSARRGREILLGPADGMVSKGWRLLAPITAYAQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                                                         ILLMCAVHPTLVFDITKLLLAVFGPLWILQASLLKVFYFVRVQGLLRFCALARKMIGGHY
                                                                          GHAVGI FRAAVCTRGVAKAVDFI PVENLETTMR
                                                                                   GHAVGI FRAAVCTRGVAKAVDFI PVESMETTMR
                                                                                                       POGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPA
                                                                                                                    PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
                                                                                                                                    QVEGEV
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                   VQIVSTAAQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPA
                                      STANDARD;
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81.9%;
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Last annotation updat
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NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).

POTENTIAL.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

ATP (POTENTIAL).
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Pred. No. 5.6e
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[Contains: Capsid

(Core

protein)

EMBL; M67463; AAA4534.1; -.
pIR; A36814; GNAVCH.
pDB; 1HEI; 25-KOV-98.
pDB; 1A1V; 16-FEB-99.
pDB; 1A1R; 17-JUN-98.
MEROPS; S29.001; -.
MEROPS; U39.001; -.
TRANSFAC; T04155; -.
InterPro; IPR001410; DEAD.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_capsid.

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Kim J.L., Morgenstern K.A., Griffith J.P., Dwyer Murcko M.A., Lin C., Caron P.R.; "Hepatitis C virus NS3 RNA helicase domain with oligonucleotide: the crystal structure provides of unwinding.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21) (EC 3.4.99 -); Protease/helicase NS3 (P70) (Hepacivirin) (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein NS5B (P67); RNA-directed RNA polymerase) (EC 2.7.7.48)]. NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)]. Hepatitis C virus (isolate H) (HCV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92052256;
Inchauspe G., Zebe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic structure of the human prototype strain H of virus: comparison with American and Japanese isolates. Proc. Natl. Acad. Sci. U.S.A. 88:10292-10296(1991).
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NCBI_TaxID=11108;
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                                                                                                                                                                                                      precursor polyprotein, commonly with Asp or Glu in the P6
position, Cys or Thr in P1 and Ser or Ala in P1.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
{RNA}(N).
SUBUNT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED B
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
AND E2. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
AND E2. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
AND E3. THE STRUCTURAL PROTEINS C, E1 AND E2 ARE PRODUCED BY
PTM: THE STRUCTURAL PROTEINS C, E1 AND E2 ARE PRODUCED SY
PROTEOLYTIC PROCESSING BY THE HOST SIGNAL PEPTIDASE FAMILY U39.
SIMILARITY: THE NS3 PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256; PubMed=1658800;
Zebedee S., Lee D.H.H.,
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MBL outstation -
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Transmembrane; Nonstructural protein; Hydrolase; Serine
3D-structure.
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Pfam; PF00271; helicase C; 1.
Pfam; PF00998; viral RdRP; 1.
ProDom; PD186062; HCV NS1; 1.
SMART; SMO0487; DEXDC; 1.
SMART; SMO0487; DEXDC; 1.
Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
Core protein; Coat protein; Transferase; Polyprotein; Coat protein; Transferase; Core protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein; Coat protein
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n; PF01538; HCV_NS1; 1.
n; PF01538; HCV_NS2; 1.
n; PF01506; HCV_NS3; 1.
n; PF01000; HCV_NS4a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF00271; hellcase_C; 1.
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ENVELOPE GLYCOPROTEIN E2.
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NONSTRUCTURAL PROTEIN NS2.
PROTEASE/HELICASE NS3.
NONSTRUCTURAL PROTEIN NS48.
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                                                     PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
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Pred. No. 5.3e-134;
6; Mismatches 37;
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A Okamoto H., Okada S.-I., Sugiyama Y., Kurai K., Lizuka H.,

A Okamoto H., Okada S.-I., Sugiyama Y., Kurai K., Lizuka H.,

A Machida A., Miyakawa Y., Mayumi M.;

A Machida A., Miyakawa Y., Mayumi M.;

Proma human carrier: comparison with reported isolates for contained the sequence of the genomic RNA of hepatitis C virus in the viral RNA reported isolates for contained the sequence of the genomic NS2A, NS2B, NS4A and NS4B are contained to the sequence of four peptide bonds in the procursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosph (RNA)(N).

C -!- SUBUNIT: The virion of this virus is a nucleocapsid covered the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of t
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EIR; JQ1303; JQ1303.
HSSP; P27958; 1HEI.
MEROPS; S29.001; -.
MEROPS; U39.001; -.
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Genome polyprotein [Contains: Capsid protein C (Core protein) [P22);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.9); Nonstructural protein NS48 (P4); Nonstructural protein
NS48 (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate HC-76) (HCV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@@isb-sib.ch).
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protein M and glycoprotein E. The
protein C and mRNA.
SIMILARITY: THE PROTEASE BELONGS
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Cys Ser_trypsin.
DEAD.
HCV capsid.
HCV core.
HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS4a.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
HCV_NS4b.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e is a nucleocapsid covered
e consists of two proteins
nucleocapsid is a complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDASE FAMILY S29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NS4A and NS4B are
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Polyprotein; Glycoprotein; Transferase; RNA-directed
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prpro; IPR001650; Helicase_C
prpro; IPR007109; Peptidase_srpro; IPR007095; RNA_poll_DS
prpro; IPR007094; RNA_poll_PS
n; PF01543; HCV_capsid; 1.
n; PF01543; HCV_capsid; 1.
n; PF01539; HCV_env; 1.
n; PF01539; HCV_NS2; 1.
n; PF01589; HCV_NS2; 1.
n; PF01589; HCV_NS3; 1.
n; PF01006; HCV_NS3; 1.
n; PF01010; HCV_NS4; 1.
n; PF01010; HCV_NS4; 1.
n; PF01010; HCV_NS4b; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
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n; PF01506; HCV_NS5a; 1.
n; PF01506; HCV_NS5a; 1.
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MKLAALTGTYVYDHLTFLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIIS
                                AVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAF
                                                         GAALLVLITLFTLTPGYKTLLSRFLWWLCYLLTLAEAMVQEWAPPMQVRGGRDGIIWAVA
                                                                          GGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTC
                       IFCPGVVPDITKWLLAVLGPAYLLKGALTRVPYFVRAHALLRMCTMVRHLAGGRYVOMVL
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ncv NS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coat
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nonstructural
                                                                                                                              AA:
                                                                                                                                     protein;
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; RNA_pol_DS_PS.
; RNA_pol_PSvir.
                                                                                                    68.3%;
                                                                                                                              329165
                                                                                          58;
                                                                                                                                                                                                                                                                                                                                                        CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN C (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE, HELICASE NS3 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
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1 protein; Hydrolase; Serine pro
REMOVED FROM CAPSID PROTEIN C
                                                                                          Score 1403; D
Pred. No. 1.3e
8; Mismatches
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CHARGE RELAY SYST
CHARGE RELAY SYST
ATP (POTENTIAL).
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POLG_HCVJ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Genome polyprotein E1 (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein Protein NS3 (P70) (Hepactvirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Heparitis C virus (isolate HC-J8) (HCV).
Heparity SRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                         EMBL; D10988; BAA01761.1;
PIR; A40250; GNWVJ8.
                                                                                                                                                                                                                                                                                                   protein M and glycoprotein E. The nucleocapsid is a compl protein C and mRNA.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=92330232; PubMed=1314459;
Ckamoto H., Kurai K., Okada S.-I., Yamamoto K., Lizuka
Fukuda S., Tsuda F., Mishiro S.;
"Full-length sequence of a hepatitis C virus genome hav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLG_HCVJ8
P26661;
                                 MEROPS; S29.001; -. MEROPS; U39.001; -.
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Full-length sequence of a hepatitis C virus genome having poor homology to reported isolates: comparative study of four distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepacivirus.
NCBI_TaxID=11115;
 InterPro; IPR001410;
                                                                       HSSP; P27958; 1HEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. and NS5 may play a role in the viral RNA replication. CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viprecursor polyprotein, commonly with Asp or Glu in the P6 position. Cys or Tar in p1 and Ser or Ala in P1'.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188:331-341(1992).
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Best Local s
Matches 246
                                                                                                                                                                                                                                                                                                                                                                                                 W Polyprotein; January 1.

W Polyprotein; Coat protein; Envelope protein; Helicase; ATP-binding;
W Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
W Transmembrane; Nonstructural protein; Hydrolase; Serine protease.
INIT_MET 1 15 CARNOVED FROM CAPSID PROTEIN C BY THE
CHAIN 116 191 MATRIX PROTEIN (POTENTIAL).
T CHAIN 192 383 MATRIX PROTEIN (POTENTIAL).
T CHAIN 384 733 NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
T CHAIN 384 733 NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
T CHAIN 1650 1866 NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
T CHAIN 1667 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 2018 3033 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
T CHAIN 1867 2017 NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
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Pfam; PF01543; HCV core; 1.
Pfam; PF01543; HCV core; 1.
Pfam; PF01560; HCV NS2; 1.
Pfam; PF01560; HCV NS2; 1.
Pfam; PF01006; HCV NS3; 1.
Pfam; PF01001; HCV NS4; 1.
Pfam; PF01001; HCV NS4; 1.
Pfam; PF01001; HCV NS4; 1.
Pfam; PF01506; HCV NS3; 1.
Pfam; PF01960; HCV NS3; 1.
Pfam; PF01960; HCV NS3; 1.
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); IPR002521; HCV_core.
); IPR002531; HCV_env.
); IPR002531; HCV_NS1.
); IPR002531; HCV_NS4.
); IPR00145; HCV_NS4a.
); IPR001490; HCV_NS4b.
); IPR002868; HCV_NS4b.
); IPR002868; HCV_NS4b.
); IPR002109; PCT_NS4b.
); IPR002109; RNA_DOL_DS PS.
); IPR007095; RNA_DOL_PSVir.
701543; HCV_capsid; 1.
                                                      Similarity
GLAILVIISIFTLTPAYKILLSRSVWWLSYMLVLAEAQIQQWVPPLEVRGGRDGIIWVAV 882
               GGAVFIGLALLTLSPYYKVLLARLIWMLQYLITRVEAHLQVWIEPLNVRGGRDAIILLTC 65
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Query Match
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Matches 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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P29326;
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                                                   SEQUENCE
                                                                                                             InterPro; IPR004261; SP2. InterPro; IPR008975; Viral
                                                                                                                                     EMBL; M73218; AAA45736.1; -. PIR; C40778; VHWWH2.
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Virology 185:120-131(1991).
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                                                                                                  Pfam; PF03014; SP2; 1.
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, 70978 MW;
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   52;
 Score 102.5; 1
Pred. No. 1.1;
52; Mismatches
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76 82;

TKLLL--AIFGPLMVLQAG---

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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Pakistan) (HEV).
Viruses, SERNA positive-strand viruses, no DNI
Hepatitis E-like viruses.
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                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J., Malik I.A., Iqbal M., Purcell R.H.;

"Characterization of a prototype strain of hepatitis E virus.";

Proc. Natl. Acad. Sci. U.S. A. 89:559-563(1992).

-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RU
                                                                                                                                EMBL; M80581; AAA45727.1; -.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=92115700; PubMed=1731327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=33774;
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                   Score 102.5;
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RESULT
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                                         MEDLINE=86200215; PubMed=3009829;
Balgarno L., Trent D.W., Strauss J.H., Rice C.M.;
"Partial nucleotide sequence of the Murray Valley encephalitis virus genome. Comparison of the encoded polypeptides with yellow fever virus structural and non-structural proteins.";
J. Mol. Biol. 187:309-323(1986).
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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InterPro, IPR007110; g-like.
InterPro, IPR007110; g-like.
InterPro, IPR001850; Peptidase_S7.
Pfam; PF002832; Flavi_capsid; 1.
Pfam; PF00869; Flavi_glycoprot; 1.
Pfam; PF00949; Flavi_helicase; 1.
Pfam; PF001004; Flavi_NS1; 1.
Pfam; PF001005; Flavi_NS2; 1.
Pfam; PF001005; Flavi_NS2; 1.
Pfam; PF01007; Flavi_propep; 1.
Pfam; PF0107; Flavi_propep; 1.
Pfam; PF0107; Flavi_propep; 1.
ProDom; PD001556; Flavi_NS1; 1.
ProDom; PD001496; Flavi_NS1; 1.
ProDom; DD001496; Flavi_NS1; 1.
ProDom; D001496; Plavi_NS1; 1.
ProDom; D001496; Plavi_NS1; 1.
ProDom; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D001496; D00149
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o; IPR001122; Flavi_capsidC.
o; IPR000336; Flavi_dlycoprotE.
o; IPR001157; Flavi_M.
o; IPR001157; Flavi_MS1.
o; IPR000752; Flavi_NS2B.
o; IPR000487; Flavi_NS2B.
o; IPR002535; Flavi_propep.
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STANDARD; PRT; 564 AA.

PRT07; 082570;

101-0CT-1994 (Rel. 30, Created)

11 101-0CT-1994 (Rel. 30, Last sequence update)

12 11-MAR-2004 (Rel. 43, Last annotation update)

13 Signal recognition particle 54 kDa protein, chloroplast precursor

15 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

18 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

19 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

20 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

21 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

22 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

23 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

24 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

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26 (SRP54) (54 Chloroplast protein) (54CP) (FFC).

27 (SRP54) (54 Chloroplast protein) (54CP) (FFC).
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Best Local
MEDLINE-21016721; PubMed=11130714;

MEDLINE-21016721; PubMed=11130714;

Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Kohara M., Naruo K., Okumura S., Shinpo S., Takeuchi C., Watwatanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M., Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M., Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
                                                                                                                                                                                                                                                                                                                                                     Amin P., Sy D., Pilgrim M., Parry D.H., Hoffman N.E., "Isolation of two Arabidopsis mutants in the nuclear encoding the 54 kDa subunit of chloroplast signal rec
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Franklin A.E., Hoffman N.E.;
"Characterization of a chloroplast ho
the signal recognition particle.";
J. Biol. Chem. 268:22175-22180(1993).
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MEDLINE=94012817; PubMed=8408079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCA
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                                                                                                                                                                                                                                      FROM N.A
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                                                                                                                                                                                                                 Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -RGILG---
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Pred. No. 4.4;
49; Mismatches
                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                           ear gene ffc, recognition
                                                                                            Kawashima K.,
akayama S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                      Wada
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유정

VHDELVKLMGGEVSELQFAKSGPTVILLAGLQGVGKTTVCAKLACYLKKQG--KSCMLI-

Matches

Conservative

Mismatches

Indels

42;

Gaps

67

VHPELI ----FDITKLLLAIFGPLMVLQAGI--

-TKVPYFVRAQGLIRACMLVR

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RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,

RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,

RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,

Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,

RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,

RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,

RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,

RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,

RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,

RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,

RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,

RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,

RA Ramsperger U., Wedler H., Bahke K., Wedler E., Peters S.,

RA Ramsperger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

RA Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

RA Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,

RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.;

"Sequence and analysis of chromosome 5 of the plant Arabidopsis
Query Match
Best Local :
                                                                                                                                                                                                                                                                                        HSSP; 007347; 1FFH.
INCEPTO; IPR003593; AAA ATPase.
InterPro; IPR00397; SRP54.
InterPro; IPR004125; SRP54 SPB.
InterPro; IPR004780; SRP_sub.
Pfam; PF00448; SRP54; 1.
Pfam; PF002881; SRP54; 1.
Pfam; PF02978; SRP54; 1.
Pr0Dom; PD000819; SRP54; 1.
                                              DOMAIN
DOMAIN
NP_BIND
NP_BIND
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:823-826(2000).

-i- FUNCTION: May target chloroplast proteins to eithe:
or envelope membranes.

-i- SUBCELLULAR LOCATION: Chloroplast stroma.
-i- TISSUE SPECIFICITY: Most abundant in green shoot t:
lower levels seen in the roots and etiolated buds.
-i- SIMILARITY: Belongs to the GTP-binding SRP family.
                                                                                                                                                                                                                                           SMART; SM00382; AAA; 1.
TIGREAMS; TIGR00959; ffh; 1.
PROSITE; PS00300; SRP54; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z21970; CAA79981.1; -.
EMBL; AF092168; AAC64139.1;
EMBL; AL162873; CAB85514.1;
                                                                                                                                                                                                                           Signal
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                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S36637; S36637.
                                                                                                                                                                                                                             recognition
 Similarity
                                                                 76
371
183
265
323
                                    370
564
190
269
326
76
61232 MW;
                                                                                                                                                                                                                             particle;
   26.1%;
                   4.9%;
                                                              M-DOMAIN.
GTP (BY S
GTP (BY S
GTP (BY S
 Score 101;
Pred. No. 1.
                                                                                                                                                               SIGNAL RECOGNITION PROTEIN.
                                                                                                                                                                                                                             GTP-binding; RNA-binding; Chloroplast;
                                              GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
E -> V (IN REF. 2).
423F7285FB9063E4 CR
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                   DB
                                                   CRC64;
               Length
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                                                                            Query Match
Best Local S
Matches 55
                                                                                                                                                                                InterPro; IPRO07200; DNA_pol_alpha_B.

Pfam; PF04058; DNA_pol_alpha_B; 1.

DNA_replication; Nuclear profile; Phosphorylation.

DOMAIN 101 107 POLY-GLU.

DOMAIN 115 157 PRO/SER/THR-RICH (HYD
SEQUENCE 600 AA; 66267 MW; 79F94BE6EF33FEBC CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 84-102; 269-285
MEDLINE=93216788; PubMed=8463324;
Miyazawa H., Izumi M., Tada S., Takada R., Masutani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28,
01-FEB-1994 (Rel. 28,
30-MAY-2000 (Rel. 39,
DNA polymerase alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of the cDNAs for the four subunits of mc polymerase alpha-primase complex and their gene expression cell proliferation and the cell cycle.";
J. Biol. Chem. 268:8111-8122(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPO2_MOUSE
P33611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cycle. The largest subunit (subunit A) has DNA polymerase activity, the two smallest subunits (subunits C and D) have DNA primase activity. Subunit B binds to subunit A. SUBCELLULAR LOCATION: Nuclear.

SUBCELLULAR LOCATION: Nuclear.

PTM: PHOSPHORYLATED IN A CELL CYCLE-DEPENDENT MANNER, IN G2/M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: May play an essential role at the early stage chromosomal DNA replication by coupling the polymerase alpha/primase complex to the cellular replication machine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: DNA polymerase alpha-primase is a for (subunits A, B, C and D), which is assembled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the DNA polymerase alpha subunit B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                                                                                                                                                                                                                    MGI:99690; Pola2.
                                                                                                                                                                                                                                                                                                                                                                                 B46642;
                            105
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                                                                                                                                                                                                                                                                                                                                                                                                       D13546;
                                                                            l Similarity
55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        s requires a license agreement (S an email to license@isb-sib.ch).
LIRACMLVRKAAGGHYVQM-AFMKLAALT-----GTYVYDHL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAAGGHYVQMAFMKLAAL---TGTYVYDHLTPLQ--DWAHAGLRDLAVAVEPVIFSDMEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GITGAILTKLDGDSRGGAALSVKEVS
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                              B46642
                                                                                                                                                                                                                                                                                                                                                                                                     BAA02746.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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28, Last sequence update)
39, Last annotation updat
pha 70 kDa subunit (DNA pc
                                                                                                      4.9%;
                                                                            34;
                                                                            Score 101; DB
Pred. No. 1.3;
34; Mismatches
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takada R., Masutani M.,
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                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               machinery
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                                                                               62;
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                            --TPLODWA
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                                                                                                                                                                                                                                                                          RA Simpson A.J.G., Resinach F.C., Arrida P., Abreu F.A., Acencio M., RA Alvarenga R., Alvee L.M.C., Arrya J.E., Baia G.S., Baptista C.S., RA Alvarenga R., Alvee L.M.C., Arrya J.E., Baia G.S., Baptista C.S., RA Barros M.H., Benaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S. RA Barros M.H., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa M.R.R. Coutinho L.L., Cristofani M., Dias. Neto E., Docena C., El-Dorry H., RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., RA Fraga J.S., Kuramae E.E., Laigref F., Lambais M.R., Lente L.C.C., RA Lente E.G.M., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V.F., Lopes S.A., Lopes C.R., Machado J.A., RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Marcins E.A.L., Martins E.M.F., Marino C.L., Manyaki C.Y., Monteiro-Vicorello C.B., RA Mond D.H., Magai M.A., Nascimento A.L.T.O., Netto L.E.S., RA Mond D.H., Magai M.A., Nascimento A.L.T.O., Netto L.E.S., RA Mania A. Jr., Dereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., RA de Silva M.C., da Silva A.M., da Silva F.R., Silva W.A. Jr., RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., RA da Silva A.F., Santelli R.V., Sawasaki H.E., de Souza A.P., Terenzi M.F., Triffi D., Tsai S.M., Tsuhako M.H., Whish M.A., Van Shuys M.A., Verjovski-Almeida S., Vettore A.L., "The Commons of the nint pathogen Xviella fastidiosa.":
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_YA47_
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Q9PEI1;
28-FEB-2003
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                                                                                                                                                                                                                                             "The genome sequence of the Nature 406:151-159(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Xanthomonadaceae; Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical XF1047.
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                                                                                                                                                                                                           COFACTOR: Zinc (Probable).
SUBCELLULAR LOCATION: Inte
                                                                                                                                                   SIMILARITY: Belongs to peptidase SIMILARITY: Contains 1 PDZ/DHR dc
                                                                                                                                                                                           (By similarity)
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                                                                                                                                                                                                             Integral membrane
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Xf1047 (EC
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Matches 64
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InterPro; IPR004387; Pept M50 Zn.
InterPro; IPR008025, Pept M Zn BS.
InterPro; IPR008915; Peptidase M50.
Pfam; PP02163; Peptidase M50; T.
SWART; SW00228; PDZ; Z.
TIGRFAMs; TIGR00054; TIGR00054; 1.
                                                                                                                     CYAA LEIDO STANDARD; PRT; 1380 AA (27675; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation updat (Receptor-type adenylate cyclase A (EC 4.6.1 1 ) (Adenylyl cyclase).
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                                                                               Leishmania donovani.
Eukaryota; Euglenozoa;
NCBI_TaxID=5661;
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PROTEASE; 1.
Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003942;
PIR; G82728; G82
MEROPS; M50.004;
           STRAIN=1S Sudanese;
MEDLINE=95340554; PubMed=7615561;
Sanchez M.A., Zeoli D., Klamo E.M., Kavanaugh M.P., Lan
"A family of putative receptor-adenylate cyclases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                            SEQUENCE FROM N.A.
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                                                                                               Kinetoplastida;
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Pred. No. 3
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4.6.1.1)
                                                                                               Trypanosomatidae;
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              Landfear S.M.;
rom Leishmania
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Best Local :
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SMART; SM00044; CYCC; 1.

PROSITE; PS50125
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Membrane-bound.
-!- DEVELOPMENTAL STAGE: Expressed in the insect stage (promastigote)
but not in the mammalian host stage of the parasite life cycle.
-!- SIMILARITY: Belongs to the adenylyl cyclase class-3 family.
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METAL
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Lyase; cAMP biosynthesis; Transmembrane; Receptor; Glycoprotein;
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                                                                                                                                                                         GWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGE----VQVVSTATQSFLATCVNGV
                                                                                                                                                                                                                                                                                 LAALTG-----TYVYDHLTPLQDWAHAGLRDLAVA-VEPVIFSDMEVK------
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                                                                                                                        CWTVFHGAGSKTLAGPK----GPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLV
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                                                                                                                                                                                                                               ----IITWGADTAACGDIISGLPVSARRGREILLG---
                                                                                                                                                                                                                                                        ---LTGMHFGGEELTYVQDTLTSL-----LRDPAVLYTVPYSESSVEVDEEAFDAMAD
                        AKAV--
                                               TLEQTDWIVNRSTYKAGLENONREVIGGDYVLGDYGGP--CEPLAOFLG--ASCYCNOGG
                                                                         TRHADVIPVRRRGDSRGSLLSPRPV---SYLKGSSGGPLLC-PSGHAVGIFRAAVCTRGV
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ITY: ATP = 3',5'-cyclic AMP + diphosphate.
I magnesium ion per subunit (By similarity)
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                       DFIPVESME
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Pred. No. 1
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Search completed: May 6, 2004, 09:31:50 Job time: 9.20459 secs

Page 16

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R MEROPS; S29.001; -.

R MEROPS; S29.001; -.

R MEROPS; U39.001; -.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019031; C:viral envelope; IEA.

R GO; GO:0009524; F:AIP binding; IEA.

R GO; GO:0000524; F:AIP binding; IEA.

R GO; GO:0005489; F:electron transporter activity; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0003526; F:serine-type peptidase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9J3F9;
                                                                                                                                         progression.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
IS UBLUIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MENNA (BY SIMILARITY).

EMBL; AF207774; AAF65964.1; -.
EMBL; A61196; A61196.
PIR; PS0329; PS0329.
                                                                                                                                                                                                                                                                                                                                       Genome polyprotein.
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                           Nagayama K., Kurosaki M., Enomoto N., "Characteristics of hepatitis C viral
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=MD33;
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                                                                                                               PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
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IPR000345; CytC_heme_BS.
IPR001410; DEAD.
IPR002522; HCV_capsid.
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R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0019028; C:viral capsid; IEA.
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R GO; GO:0019021; C:viral envelope; IEA.
R GO; GO:0019025; F:ATP binding; IEA.
R GO; GO:000524; F:ATP binding; IEA.
R GO; GO:000325; F:ATP dependent helicase activity; IEA.
R GO; GO:000549; F:electron transporterase activity; IEA.
R GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO:0003965; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO:0003965; F:serine-type peptidase activity; IEA.
R GO; GO:0008219; F:structural molecule activity; IEA.
R GO; GO:0005199; F:structural molecule activity; IEA.
R GO; GO:0006104; F:teransferase activity; IEA.
R GO; GO:0006104; F:electron transport; IEA.
R GO; GO:0006109; F:electron transport; IEA.
R GO; GO:0006509; P:proteolysis and peptidolysis; IEA.
R GO; GO:001907; P:viral genome replication; IEA.
R GO; GO:001907; P:viral transformation; IEA.
R GO; GO:001907; P:viral transformation; IEA.
                                             Pfam; PF01543; HCV_capsiā; 1
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01538; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF01038; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
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Hepatitis C virus..
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Q9J3H7;
Q1-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2003 (TrEMBLrel. 25,
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Submitted (NO
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NCBI_TaxID=11103;
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P; P26663; 1JXP.
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEARSID COVERED BY
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSIGTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).
                                                                                                                                                                                                                                         b; IPR009003; Cys Ser_tryps
c; IPR000345; CytC heme_BS.
c; IPR000345; CytC heme_BS.
c; IPR002522; HCV_capsid.
c; IPR002521; HCV_core.
c; IPR002521; HCV_core.
c; IPR002519; HCV_MS1.
c; IPR002518; HCV_MS1.
c; IPR002518; HCV_MS2.
c; IPR000745; HCV_MS4a.
c; IPR000746; HCV_MS4a.
c; IPR002868; HCV_MS4a.
c; IPR002868; HCV_MS5a.
c; IPR002166; HCV_RGRP.
                                                                                                                                                                                 ; Peptidase C29.; RNA_pol_DS_PS.; RNA_pol_PSvir.
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"Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients at "Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients at the hepatocellular carcinoma: the 'progression score' revisited.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

CC PROTEIN GENELON OF THIS VIRUS IS A NUCLEOCAPSID EN A LIPOPROTEIN ENVELOPE. THE SUNGLOPE CONSISTS OF TWO PROTEINS:

CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF THE PROTEIN GRAPH AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF THE PROTEIN FOR PROTEIN GAND MRNA (BY SIMILARITY).

REBL, ABG196; A61196.

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REPLR; A66196; A61196.

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01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
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Coat protein; Envelope protein; Glycoprotein; Nonstructural Polyprotein; RNA-directed RNA polymerase; Transferase; Transsequence 3010 AA; 327365 MW; D8653F7317FFA106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome polyprotein. Hepatitis C virus.
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NCBI_TaxID=11103;
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Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K
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Hijikata M.,
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InterPro; IPR00345; CytC heme BS.
InterPro; IPR003410 DEAD.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_env.
InterPro; IPR002513; HCV_NS1.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002531; HCV_NS4.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR00166; HCV_NS4b.
InterPro; IPR00166; HCV_NS4b.
InterPro; IPR00166; HCV_NS4b.
InterPro; IPR001669; HCV_NS4b.
InterPro; IPR001690; HCV_NS4b.
InterPro; IPR001690; HCV_NS4b.
InterPro; IPR001690; HCV_NS4b.
InterPro; IPR001650; HCV_NS4b.
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InterPro; IPR001650; HCV_NS4b.
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SMART; SM00490; HELICC; 1.
SMART; SM00490; CYTOCHROME_C; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
ATP-binding; Coat protein; Envelope protein; Glycoprotein;
ATP-binding; Coat protein; Polyprotein;
Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Transferase; Transmembrane.
RNA-directed RNA polymerase; 3010 AA; 327042 MW; 3807DC6879684C95 CRC64;
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GO:0003723; F:RNA binding; IEA.
GO:0003768; F:RNA-directed RNA polymerase activity;
GO:0008236; F:serine-type peptidase activity; IEA.
GO:0005198; F:structural molecule activity; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0006118; P:electron transport; IEA.
GO:0006350; P:proteolysis and peptidolysis; IEA.
GO:0006350; P:transcription; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO: 0019079; P: viral genome replication; IBA.
                                                                                                1054
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                                          301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
         PPGARSMTPCTCGSSDLYLVTRHÅDVIFVRRRGDSRGSLLSPRPVSYLKGSSGGFLLCPS
                                                                                             QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA
                                                                                                                                                                                                               GDIISGLFVSARRGREILLGPADSLEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                                                                                                                                                                                                                                                                                                     VQMAFMKLAALTGTYVYDHLTPLRDWAHTGLRDLAVAVEPVVFSDMETKI ITWGADTAAC
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Pred. No. 2.1e-156;
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PPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS

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                              InterPro; IPR002521; HCV core.
InterPro; IPR002513; HCV env.
InterPro; IPR002514; HCV NS1.
InterPro; IPR002518; HCV NS2.
InterPro; IPR002518; HCV NS4a.
InterPro; IPR002518; HCV NS5a.
InterPro; IPR002686; HCV NS5a.
InterPro; IPR00266; HCV NS5a.
InterPro; IPR002166; HCV RdRp.
InterPro; IPR001650; HelTcase C.
InterPro; IPR004109; Peptidase C.
InterPro; IPR004109; Poptidase C.
InterPro; IPR004109; RNA pol DS InterPro; IPR007094; RNA pol DS InterPro; IPR007094; RNA pol DS InterPro; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; IPR007094; RNA pol DS INTERPO; INTERPO; IPR007094; RNA pol DS INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERP007094; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; INTERPO; IN
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-i- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN ENVELOPE CONSISTS OF TWO PROTEIN C AND MRNA (BY SIMILARITY).

EMBL, A8049101; BAB1814.1; -.

EMBL, A8049010; BAB18814.1; -.

EIR; P00246; P00246.

PIR; P00246; P00246.
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InterPro;
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GO; GO:0019028; C:virial capsid; IEA.
GO; GO:0019031; C:virial capsid; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0003968; F:serine-type peptidase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:stransferase activity; IEA.
GO; GO:0005198; P:ptransferase activity; IEA.
GO; GO:0006508; P:ptransferase activity; IEA.
GO; GO:0006509; P:transferase activity; IEA.
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01-MAR-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K.,
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NCBI_TaxID=11103;
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Hepatitis C virus.
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                                                                                                                                                                                                                                                  ); IPR009003; Cys_Ser_trypsin.
); IPR001345; CytC_heme_BS.
); IPR001410; DEAD.
); IPR002522; HCV_capsid.
); IPR002521; HCV_core.
); IPR002521; HCV_core.
); IPR002531; HCV_NS1.
); IPR002518; HCV_NS2.
); IPR000745; HCV_NS4a.
); IPR000745; HCV_NS4a.
); IPR001966; HCV_NS4A.
); IPR002166; HCV_NS4ARP.
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P:viral genome replication; IEA.
P:viral transformation; IEA.
                                                                                                    HelTcase_C.
Peptidase_C29.
RNA_pol_DS_PS.
RNA_pol_PSvir.
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Hijikata M.,
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RESULT 5
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PR Pfam; PF01538; HCV_NS2; 1.

PR Pfam; PF01538; HCV_NS4; 1.

Pfam; PF01006; HCV_NS4a; 1.

Pfam; PF01001; HCV_NS4b; 1.

Pfam; PF01001; HCV_NS4b; 1.

Pfam; PF01506; HCV_NS5a; 1.

Pram; PF00271; helicase C; 1.

Pfam; PF00298; Viral RdRP; 1.

Pr Pfam; PF00998; Viral RdRP; 1.

ProDom; PD186062; HCV_NS1; 1.

ProDom; SMATT; SM00487; DENDC; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; PS00190; CYTOCHROME C; 1.

PROSITE; SM00487; DENDEJOR protein; Glycoprotein; Helicase; WHYdrolase; Monstructural protein; Polyprotein;

RNA-directed RNA polymerase; Transferase; Transmembrane.

SEQUENCE 3010 AA; 327108 MW; DE182D810EF78EE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 96.2%;
Best Local Similarity 94.9%;
Matches 373; Conservative
Mishiro S.;

"Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients "Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients with hepatocellular carcinoma: the 'progression score' revisited.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

1- SUBGNUT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENTHE NUCLEOCAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                            01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                            Genome polyprotein.
Hepatitis C virus.
                                                                                                                  Takahashi K., Iwata K
Hatahara T., Ohta Y.,
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01-MAR-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                      Takahashi K.,
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                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=11103;
                                                                                                                                                                                                                           Hepacivirus.
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                                                                                                                     K., Matsumoto M., Matsumoto H., ., Kanai K., Maruo H., Baba K., 1
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Pred. No. 5.4e-156;
B; Mismatches 12;
                                                                                                                                                                                                                                             viruses,
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Hijikata M.,
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Best Local S
Matches 371
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GG; GG:0019087; P.viral transformation; IEA.
InterPro; IPR00903; CyG Ser trypsin.
InterPro; IPR000345; CyC_heme_BS.
InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_core.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_core.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002531; HCV_NS3.
InterPro; IPR002531; HCV_NS4A.
InterPro; IPR002588; HCV_NS4A.
InterPro; IPR002688; HCV_NS5A.
InterPro; IPR002688; HCV_NS5A.
InterPro; IPR002688; HCV_NS5A.
InterPro; IPR002688; HCV_NS5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00487; DEXDC; 1.

PROSITE; PS00190; CYTOCCHROME C; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural Polyprotein; RNA-directed RNA polymerase; Transferase; Trans SEQUENCE 3010 AA; 327324 MW; 3DE6CF249BD1151C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0010021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000549; F:ATP binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003968; F:structural molecule activity; IEA.
GO; GO:0003968; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:00010740; F:transferase activity; IEA.
GO; GO:0005198; P:proceedlysis and peptidolysis; IEA.
GO; GO:0005198; P:proceedlysis and peptidolysis; IEA.
GO; GO:0005350; P:transcription; IEA.
GO; GO:0005350; P:transcription; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
TIPED000073. Cvs Sear trunsin
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SMART; SM00487;
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                             VQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
                                                                                                                                                                                                MAASCGGAVFVGLALLTLSPYYKVFLARLIWWLQYLLTRAEAHLQVWVPPLNVRGGRDAI
                                                                                                                                                                                                                           MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
                                                                                           VQMAFMKLAALTGTYVYDHLTPLQDWAHASLRDLAVAVEPVVFSDMETKIITWGADTAAC
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                                                                                                                                                                                                                                                                                                                      96.1%;
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Pred. No. 6.6e-156;
1; Mismatches 11;
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Go; Go:0019028; C:viral capsid; IEA.
Go; Go:0019031; C:viral capsid; IEA.
Go; Go:0005524; F:ATP binding; IEA.
Go; Go:0005524; F:ATP binding; IEA.
Go; Go:0000548; F:ATP binding; IEA.
Go; Go:00003723; F:RNA binding; IEA.
Go; Go:0003723; F:RNA binding; IEA.
Go; Go:00005136; F:serine-type peptidase
Go; Go:0000518; P:serine-type peptidase
Go; Go:0000518; P:serine-type peptidase
Go; Go:000518; P:serine-type peptidase
Go; Go:000518; P:serine-type peptidase
Go; Go:000519; P:stranscription; IEA.
Go; Go:0006350; P:transcription; IEA.
Go; Go:0006350; P:transcription; IEA.
Go; Go:0019079; P:viral genome replicat.
Go; Go:0019087; P:viral genome replicat.
Go; Go:0019087; P:viral transformation;
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR0005521; HCV_core.
InterPro; IPR007522; HCV_core.
InterPro; IPR007523; HCV_NS4a.
InterPro; IPR007531; HCV_NS4a.
InterPro; IPR007149; HCV_NS4a.
InterPro; IPR007149; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR007166; HCV_NS4a.
InterPro; IPR0
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Q807P3;
01-JUN-2003
01-JUN-2003
01-OCT-2003
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Kishine H., Sugiyama K., Hijikata M., Kato N., Ta
Nio Y., Hosaka M., Miyanari Y., Shimotohno K.;
"Subgenomic replicon derived from a cell line inf
hepatitis C virus.";
Biochem. Biophys. Res. Commun. 293:993-999(2002).
EMBL, AB080299; BAC54896.1; -.
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GO; GO:0019021; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP dependent helicase activity; IEA.
GO; GO:000326; F:ATP dependent helicase activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA directed RNA polymerase activity; IEA.
GO; GO:0003968; F:serine-type peptidase activity; IEA.
GO; GO:0005198; F:serine-type peptidase activity; IEA.
GO; GO:0005198; F:serine-type peptidase activity; IEA.
GO; GO:0006518; P:electron transport; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006509; P:transcription; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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25,
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Last sequence update)
Last annotation updat
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Matches 372; Conserv
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Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS5a; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF00279; helicase C; 1.
Pfam; PF00998; Viral RdRP; 1.
ProDom; PF00998; Viral RdRP; 1.
PRART; SM00480; HELICC; 1.
                                                                                                                                                                                                                                          Q9J3H3;
Q9J3H3;
01-OCT-2000
                                                                                                 STRAIN=MD19;
Nagayama K., Kurosaki M., Enomoto N.,
"Characteristics of hepatitis C viral
                                                                                                                                                                        Genome polyprotein.
Hepatliis C virus.
Viruses; SERNA positive-strand
Hepacivirus.
                                                                                 progression.";
Submitted (NOV
                                                                                                                                                                                                                      01-OCT-2000
01-OCT-2003
                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00190; CYTOCHROME_C;
                                                                                                                                                             ICBI_TaxID=11103;
mitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA (BY SIMILARITY).

L; AP207780; AAP865950.1; -.

; A61196; A61196.
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                                                                                                                                                                                                                                                                                                                          GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 1206
                                                                                                                                                                                                                                                                                                                                          GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
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Pred. No. 6.6e-156;
9; Mismatches 12;
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annotation update)
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000549; F:ATP binding; IEA.
GO; GO:0003793; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA birected RNA polymerase activity; IEA.
GO; GO:0003968; F:scrine-type peptidase activity; IEA.
GO; GO:0003968; F:scrine-type peptidase activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:transferase activity; IEA.
GO; GO:0005198; P:electron transport; IEA.
GO; GO:0006518; P:electron transport; IEA.
GO; GO:0006530; P:transcription; IEA.
GO; GO:0006530; P:transcription; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
GO; GO:0019087; P:viral genome replication; IEA.
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OVEGEVOVVSTATOSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYINVDQDLVGWQA
                                                                          VQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVBPVIFSDMEVKIITWGADTAAC
                                                                                                        TLLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY
                                                                                                                                   MAASCGGAVFIGLALLTLSPHYKVFLARLIWWLQYFITRVEAHLHVWVPPLNVRGGRDAI
                           GDIILGLPVSARRGKEIFLGPADNLEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDRN
                                    GDIISGLÞVSARRGREIILGÞADNFEGQGWRLLAÞITAYSQQTRGLLGCIITSLTGRDKV
                                                                                               ILLTCAVHPELIFSITKILLAIFGPLMVLQAGITRVPYFVRAQGLIRACLLARKVAGGHY
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Pred. No. 9.7e
14; Mismatches
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L. J. Biochem. 118:1199-1204(1995).
C. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVE
C. LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTE
C. PROTEIN C AND MRNA (BY SIMILARITY).
C. EMBL; D45172; BAA08120.1; -.
R. PIR; A61196; A61196.
R. PIR; P20246; P00246.
R. PIR; P20663; 10XP.
R. FIR; P20663; 10XP.
R. GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019026; F:AITP binding; IEA.
GO; GO:000973; F:RNA binding; IEA.
GO; GO:000973; F:RNA binding; IEA.
GO; GO:000973; F:RNA binding; IEA.
GO; GO:000973; F:RNA binding; IEA.
GO; GO:0009836; F:RNA binding; IEA.
GO; GO:0009836; F:RNA binding; IEA.
GO; GO:0009836; F:RNA binding; IEA.
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GO; GO:0009836; F:RNA binding; IEA.
GO; GO:0009836; F:RNA binding; IEA.
GO; GO:0009987; F:VITABISTIAN DEPLICATION; IEA.
GO; GO:0019087; P:VITABISTIAN TEAL
GO; GO:0019087; P:VITABISTIAN TEAL
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); IPR001410; DEAD.
); IPR002521; HCV_capsid.
); IPR002521; HCV_core.
); IPR002519; HCV_env.
); IPR002519; HCV_MS1.
); IPR002518; HCV_MS1.
); IPR00745; HCV_MS4a.
); IPR001490; HCV_MS4b.
); IPR001868; HCV_MS4b.
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Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00998; Viral_RdRP; 1.
ProDcm; PD186602; HCV_NS1; 1.
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SMART; SM00487; DEXDC; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Coat protein; Envalope protein; Glycoprotein; Transferase; Transmembrane. Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane. SEQUENCE 3010 AA; 326880 MW; EED840E6A050E766 CRC64;
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                  GHAVGI FRAAVCTRGVAKAVDF I PVESMETTMR
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                                                              PPGARSMIPCTCGSSDLYLVIRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPS
                                                                                  PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
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MEDLINE-20044440; PubMed=+000-1000 MEDLINE-20044440; PubMed=+000-1000 Medical K., 111-1000 Medical K., 2004 Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Sugiyama Y., Kurai K., 111-1000 Miyakawa Y., Mayumi M.; Sugiyama Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Mayumi M.; Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Mayumi M.; Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Mayumi M.; Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Miyakawa Y., Kurai K., 111-1000 Miyakawa Y., Kurai K., 111-1000 Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miyakawa Miya
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Sugimura T., Shimotohno K.;
"Molecular cloning of the human hepatitis C viru
patients with non-A, non-B hepatitis.";
Proc. Natl. Acad. Sci. U.S.A. 87:9524-9528(1990)
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InterPro; IPR004109; Peptidase
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF00271; helicase_C; 1.
                    SMART; SM0048
ATP-binding;
NON_TER
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Hijikata
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                                                                                                                                                       InterPro;
InterPro;
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Hijikata M., Mizushima H., Akagi T., Mori S.,
Tanaka T., Kimura K., Shimotohno K.;
"Two distinct proteinase activities required.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92230232; PubMed=1314459;
Okamoto H., Kurai K., Okada S., Yamamoto K., Iizuka
Fukuda S., Tsuda F., Mishiro S.,
"Full-length sequence of a hepatitis C virus genome
homology to reported isolates: Comparative study of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92230206; PubMed=1314449;
Chen P., Lin M., Tai K., Liu P., Lin C., Chen D.;
"The Taiwanes'e hepatitis C virus genome: Sequence determination
"mapping the 5'termini of viral genomic and antigenomic RNA.";
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Andoh T., Yoshida I.,
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J. Virol. 65:1105-1113(1991).
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InterPro; IPR001650;
InterPro; IPR004109;
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InterPro; IPR001410;
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GO:0005524; F:ATP dependent helicase activity;
GO:0008026; F:ATP dependent helicase activity;
GO:0016787; F:hydrolase activity; IEA.
GO:0003676; F:nucleic acid binding; IEA.
GO:0008206; F:serine-type peptidase activity;
GO:0006508; P:proteolysis and peptidolysis; IEGO:0019087; P:viral transformation; IEA.
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                                          DEXDc;
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ri C., Manabe S.,
I., Okayama H.;
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, DEAD.
, HCV_NS2.
, HCV_NS4a.
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Q1-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Last sequency)
01-OCT-2003 (TrEMBLrel. 25, Last annotaty)
Polyprotein precursor (Genome polyprote:
Hepatitis C virus type 2.
Viruses; ssRNA positive-strand viruses,
SEQUENCE FROM N.A.

MEDILINE=95156583; PubMed=7853491;

MEDILINE=95156583; PubMed=7853491;

Tanji Y., Hijikata M., Satoh S., Kaneko
"Henatitis C virus-encoded nonstructual
                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILINE=94333810, PubMed=8056334;

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                                                                           MEDLINE=95056078; PubMed=7966638;
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"Hepatitis C virus polyprotein processing: kinetics
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                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=94068484;
                                                                                                                                                                                                                                                                                                                                                                 Hepacivirus.
NCBI_TaxID=40271;
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ijikata M., Mizushima H., Tanji Y.,
kagi T., Kimura K., Shimotohno K.;
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RR GO; GO:0019012; C:virion; IEA.

RGO; GO:00019012; F:ATP binding; IEA.

RGO; GO:0008026; F:ATP dependent helicase activity; IEA.

RGO; GO:0003723; F:RNA binding; IEA.

RGO; GO:0003723; F:RNA binding; IEA.

RGO; GO:0003723; F:RNA binding; IEA.

RGO; GO:0003723; F:RNA binding; IEA.

RGO; GO:0003723; F:RNA binding; IEA.

RGO; GO:0003723; F:RNA binding; IEA.

RGO; GO:0003723; F:RNA binding; IEA.

RGO; GO:0006236; F:RNA-binding; IEA.

RGO; GO:0006508; P:RNA-binding; IEA.

RGO; GO:0006508; P:RNA-binding; IEA.

RGO; GO:0006508; P:Proteolysis and peptidolysis; IEA.

RGO; GO:0006508; P:Proteolysis and peptidolysis; IEA.

RGO; GO:0006509; P:viral transformation; IEA.

RGO; GO:00019079; P:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IEA.

RGO; GO:0019087; P:viral transformation; IEA.

RGO; GO:0019087; P:viral transformation; IEA.

RGO; GO:0019087; P:viral transformation; IEA.

RGO; GO:0019087; P:viral transformation; IEA.

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RGO; GO:0019087; P:viral transformation; IEA.

RGO; GO:0019087; P:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IEA.

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RGO; GO:0019079; P:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IEA.

RGO; GO:001907999; P:viral transformation; IEA.

RGO; GO:001907999; V:viral RGO; I.

RGO; GO:0006508; P:p:viral transformation; IEA.

RGO; GO:0019079; P:viral transformation; IE
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Best Local
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SMART; SMO0487; DEXDG; 1.
Nonstructural_protein; Polyprotein; RNA-directed RNA polymerase;
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J. VVC10. 69:1575-1581(1995).
EMBL; D16435, BAA03905.1; -.
PIR; A61196; A61196.
PIR; P60246; P00246.
PIR; P60329; P80329.
HSSP; P26663; 1JXP.
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71; Conservative
GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKV
                                                                                                                                                                                                              VQMAFMKLAALTGTYVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKIITWGADTAAC
                                                                                                                                                                                                                                             VQMAFMKLAALTGTYYYDHLTBLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
                                                                                                                                                                                                                                                                                                                MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
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94.4%;
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; Pred. No. 1.20
11; Mismatches
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NS3.
NS4A.
NS4B.
NS5A.
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L.2e-155;
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          RR HSSP; P26665; LUXE:

RR GO; GO:0016021; C:integral to membrane; IEA.

RGO; GO:0019028; C:viral capsid; IEA.

RGO; GO:0019031; C:viral envelope; IEA.

RGO; GO:0005524; F:ATP binding; IEA.

RGO; GO:0005524; F:ATP dependent helicase activity; IEA.

RGO; GO:0000526; F:RNA binding; IEA.

RGO; GO:00003723; F:RNA binding; IEA.

RGO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

RGO; GO:00003968; F:structural molecule activity; IEA.

RGO; GO:00005198; F:structural molecule activity; IEA.

RGO; GO:00016740; F:transferase activity; IEA.

RGO; GO:00016740; F:transferase activity; IEA.

RGO; GO:00016740; F:transferase activity; IEA.

RGO; GO:00016740; F:transferase activity; IEA.

RGO; GO:0001670; P:viral genome replication; IEA.

RGO; GO:001670; P:viral genome replication; IEA.

RGO; GO:0019079; P:viral genome replication; IEA.

RGO; GO:0019087; P:viral genome replication; IEA.

RGO; GO:0019087; P:viral genome replication; IEA.

RGO; GO:0019087; P:viral genome replication; IEA.

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RGO; GO:0019087; P:viral gen
InterPro; IPR
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-- SUBUNIT: THE VIRLO OF THE VIRLO SIS A NUCLECCASSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA (BY SIMILARITY).

EMBL; D89872; BA114035.1; --

EMBL; D89872; BA61196.

PIR; PQ0804; PQ0804.

PIR; PQ0804; PQ0804.

PIR; PQ0804; PQ0804.

PIR; PQ0804; PQ0804.
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01-MAY-1997 (TrEMBLrel. 03,
01-CCT-2003 (TrEMBLrel. 25,
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Hepatitis C virus.
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STRAIN=type 1b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1996)
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Tanaka T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11103;
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e polyprotein).
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RESULT 12
Q9J3G
ID 399J3G
AC Q9J3G
CP 01-OC
DT 01-OC
DT 01-OC
DT 01-OC
DT Genom
OS Hepat
OC Virus
OC Hepat
CX NCBI
RN [1]
RN [1]
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RN Nagay
RT Propy
RL Subm.
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Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato Ragayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato "Characteristics of hepatitis C viral genome associated with diseas progression.";

progression.";

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

1- SUBUNIT: THE VIRTON OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:

PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MANA (BY SIMILARITY).

EMBL; AF207767; AAF65957.1;

EMBL; AF207767; AAF65957.1;
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pF01006; HCV_NS4b; 1.
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WEROÉS; 829.002; Cintegral to membrane; IEA.
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PIR; PQ0246; J
PIR; PQ0254; J
PIR; PS0329; J
                                                                                                                                                                                                                                                                                        PROSITE; PS00190; CYTOCHROME C; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural
Polyprotein; RNA-directed RNA polymerase; Transferase; Trans
POLYPROTEIN RNA 327165 MW; 74PAB6BB0F24837B CRC64;
                                                                                                874
                                                                                                                                                              814
   181
                                                                121
                                                                                                                                                                                                                           372;
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                                                                                                               ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY
                                                                                                                                                        MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
                                                  VOMAFWKLAALTGTYVYDHLTBLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC
                                                                                              GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
                                 VQMALVKLAALTGTYVYDHLAPLQHWAHAGLRDLAVAVEPVVFSDMETKIITWGADTAAC
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                         95.9%;
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Pred. No. 1.7e-155;
7; Mismatches 14;
                                                                                                                                                                                                                                                           DB 12;
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PIE, A61196; A61196.

PIE, PO0804; PO0804.

PIE, PO0804; PO0804.

PIE, PO0804; PO0804.

PIE, PS0329; PS0329.

HSSP; P26663; INS3.

GO; GO:0016021; C:viral capsid; IEA.

GO; GO:0019021; C:viral capsid; IEA.

GO; GO:0009524; F:ATP dependent helicase active company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the compan
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Q99AU2;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID PROTEIN C AND MRNA (BY SIMILARITY).

EMBL; AF33324; AAK08509.1; -

PIR; A61196; A61196.

PIR; P00246; P00246.

PIR; P00804; P00804.

PIR; P50329; P50329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               during serial passage of an infectious hepatitis C virus clone in chimpanzees."; clone in chimpanzees."; submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO PARTY OF TWO 
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"Analyses of viral sequences and virus-specific immune reduring serial passage of an infectious hepatitis C virus
                                                                                                                                                                                                                                                         HSSP; P2663; INSI.

GG; GO:0016021; C:integral to membrane; IEA.

GG; GO:0019028; C:viral capsid; IEA.

GG; GO:0019031; C:viral envelope; IEA.

GG; GO:0005524; F:ATP dependent helicase activity; IEA.

GG; GO:0005549; F:electron transporter activity; IEA.

GG; GO:0005489; F:electron transporter activity; IEA.

GG; GO:0003723; F:RNA-binding; IEA.

GG; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

GG; GO:000326; F:serine-type peptidase activity; IEA.

GG; GO:0008236; F:serine-type peptidase activity; IEA.

GG; GO:0005198; F:structural molecule activity; IEA.

GG; GO:0005198; F:structural molecule activity; IEA.

GG; GO:0006508; P:transferase activity; IEA.

GG; GO:0006508; P:proteolysis and peptidolysis; IEA.

GG; GO:0019079; P:viral genome replication; IEA.

GG; GO:0019079; P:viral genome replication; IEA.
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Thomson M., Nascimbeni M.,
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses,
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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          RESULT 14

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AC Q9DTE

AC Q9DTE

DT 01-MA

DT 01-MA

DT 01-MC

CO Wirus

OC Hepat

OC Hepat

OC NCELL

RN [1]

RP SEQUE

RC STEAL

RA Hatah

RA Mishi
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Matches 369
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InterPro; IPR002166; HCV_RdRP.
InterPro; IPR004109; PepEidase C29.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007094; RNA_pol_PSvir_Pfam; pF01542; HCV_corpsid; 1.
Pfam; pF01543; HCV_corpsid; 1.
Pfam; pF01549; HCV_env; 1.
Pfam; pF01539; HCV_env; 1.
Pfam; pF01539; HCV_NS1; 1.
Pfam; pF01539; HCV_NS1; 1.
Pfam; pF01530; HCV_NS1; 1.
Pfam; pF01530; HCV_NS3; 1.
Pfam; pF01538; HCV_NS3; 1.
Pfam; pF01001; HCV_NS4a; 1.
Pfam; pF01001; HCV_NS5a; 1.
Pfam; pF01006; HCV_NS5a; 1.
Pfam; pF01506; HCV_NS5a; 1.
Pfam; pF01506; HCV_NS5a; 1.
Pfam; pF01506; HCV_NS5a; 1.
                                                                                                                                                                                                                                                                                                                                             Q9DTD7
Q9DTD7;
01-MAR-2001
                                                                                                                                                                                                        Genome polyprotein.
Hepatitis C virus.
Viruses, seRNA positive-strand
                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00190; CYTOCHROME C; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural
Polyprotein; RNA-directed RNA polymerase; Transferase; Trans
SEQUENCE 3010 AA; 327007 MW; 053B9A653B0AB335 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD186062;
SMART; SM00487; DE
          STRAIN=HCVT217;
Takahashi K., Iwata K., Matsumoto M.,
Takahara T., Ohta Y., Kanai K., Maruo
Mishiro S.;
                                                                                                                                                          Hepacivirus.
NCBI_TaxID=11103;
                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILLTCAVHPELIFDITKLLLAILGPLMVLQAGITRVPYFVRAQGLIHACMLVRKVAGGHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
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62; HCV_NS1; 1.
; DEXDC; 1.
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25,
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Last sequence update)
Last annotation updat
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Pred. No. 2.1e-155;
3; Mismatches 11;
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                                                                                                                                                                                                                   viruses,
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                                     Matsumoto H., H., Baba K., 1
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Indels Length

0

Gaps

0

933 120 873 60

993 180 protein;

Hijikata M.,

Nakao

Flaviviridae;

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                                                                                                      InterPro; IFW007095; RNA_Dol_DS_PS.

InterPro; IFR007094; RNA_Dol_DS_PS.

DR Pfam; PF01543; HCV_capsid; 1.

PF4am; PF01542; HCV_capsid; 1.

R Pfam; PF01543; HCV_care; 1.

R Pfam; PF01539; HCV_NS1; 1.

Pfam; PF01539; HCV_NS2; 1.

Pfam; PF01539; HCV_NS2; 1.

Pfam; PF01539; HCV_NS2; 1.

Pfam; PF01500; HCV_NS3; 1.

Pfam; PF01500; HCV_NS4; 1.

Pfam; PF01000; HCV_NS4b; 1.

Pfam; PF01010; HCV_NS4b; 1.

Pfam; PF01000; HCV_NS4b; 1.

Pfam; PF01506; HCV_NS5a; 1.

Pfam; PF01506; HCV_NS5a; 1.

Pfam; PF00998; Viral RdRP; 1.

Pfam; PF00998; Viral RdRP; 1.

PFAMT; SM00487; DEXDC; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00487; DEXDC; 1.
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                                              S
                                                                  Matches
                                                                          Query Match
Best Local
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PROSITE; PS00190; CYTOCCHROME C; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural Polyprotein; RNA-directed RNA polymerase; Transferase; Trans SEQUENCE 3010 AA; 326909 MW; 5505C62EB0DA0519 CRC64;
                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
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InterPro;
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InterPro;
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PIR; A61196; A61196. 
PIR; PQ0804; PQ0804. 
PIR; PS0329; PS0329.
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                                                                  371;
           61
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                                                                           Similarity
                                                                                                                                                                                                                                                                                                     | IPR002522; HCV_capsid.
| IPR002521; HCV_core.
| IPR002519; HCV_env.
| IPR002519; HCV_NS1.
| IPR002518; HCV_NS2.
| IPR000745; HCV_NS44.
| IPR001490; HCV_NS44.
| IPR001490; HCV_NS46.
| IPR002166; HCV_RdRP.
                                         ILLTCAVHEELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY
IPR009003; Cys Ser_trypsin.
IPR000345; CytC heme_BS.
IPR001410; DEAD.
                                                                  Conservative
                                                                                                                                                                                                                                                                                   Helicase_C.
                                                                          94.4%;
                                                                          Score 1967;
Pred. No. 2
                                                                  Mismatches
                                                                           2.1e-155;
                                                                                    DB 12;
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                                                                                    Length
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Transmembrane
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RESULT 15
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MERCPS; S29.002; ...

R GG; GG:0016021; C:integral to membrane; IEA.

R GG; GG:0019028; C:viral capsid; IEA.

R GG; GG:0019031; C:viral envelope; IEA.

R GG; GG:0005524; F:ATP binding; IEA.

R GG; GG:0000525; F:ATP dependent helicase activity; IEA.

R GG; GG:0003723; F:RNA binding; IEA.

R GG; GG:0003723; F:RNA-directed RNA polymerase activity; IEA.

R GG; GG:0003528; F:structural molecule activity; IEA.

R GG; GG:0005108; F:stransferase activity; IEA.

R GG; GG:0005108; F:stransferase activity; IEA.

R GG; GG:0016740; F:transferase activity; IEA.

R GG; GG:0016508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                         EMBL; AP165059; AAD56194.1; -.
PIR; A61196; A61196.
PIR; PQ0246; PQ0246.
PIR; PQ00254; PQ0254.
PIR; PQ0804; PQ0804.
PIR; PQ0804; PQ0804.
PIR; P80329; P80329.
HSSP; P26663; 1JXP.
                                                                                                                                                                                                                                                                                                                 Submitted
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Q9QIX6;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                            Nagayama K.,
Sakamoto N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasaka
Tazawa J.i., Izumi N., Marumo F., Sato C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepacivirus.
NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                Virology
                                                                                                                                                                                                                                                                                                                                                                                                                               activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20013325; PubMed=10544098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses,
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AND MENA (BY SIMILARITY).
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13,
25,
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Last annotation updat
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pfam; pF01542; HCV_core; 1.

pfam; pF01539; HCV_env; 1.

pfam; pF01539; HCV_env; 1.

pfam; pF01539; HCV_NS1; 1.

pfam; pF01538; HCV_NS2; 1.

pfam; pF01001; HCV_NS4; 1.

pfam; pF01001; HCV_NS4; 1.

pfam; pF01596; HCV_NS4; 1.

pfam; pF01596; HCV_NS4; 1.

pfam; pF01598; Viral RdRP; 1.

pfam; pF00271; hellcase C; 1.

pfam; pF00271; hellcase C; 1.

pfam; pF00271; hellcase C; 1.

pfam; pF00298; Viral RdRP; 1.

pfam; pF00271; hellcase C; 1.

pfam; pF00278; DEXDC; 1.

pfam; pF00587; DEXDC; 1.

proDom; pD186062; HCV_NS1; 1.

SMART; SM00487; DEXDC; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.

SEQUENCE 3010 AA; 327466 MW; 4613744EC4D4A013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.8
Best Local Similarity 94.4
Matches 371; Conservative
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GO; GO:0019079;
GO; GO:0019087;
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Pfam; PF01
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InterPro;
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; IFR00252; HCV_core.
; IFR002521; HCV_core.
; IFR002511; HCV_env.
; IFR002511; HCV_NS1.
; IFR002518; HCV_NS2.
; IFR002518; HCV_NS4.
; IFR001490; HCV_NS4.
; IFR00166; HCV_RS4.
; IFR002166; HCV_RGRP.
; IFR001650; Heliase_C2.
; IFR0017095; RNA_pol_DS_PS.
; IFR007095; RNA_pol_PS_V1.
; IFR007094; RNA_pol_PS_V1.
GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
                                                      PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
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P:viral genome replication;
P:viral transformation; IEA.
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Pred. No. 2.1e-155;
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Search completed: May 6, 2004, 09:35:46 Tob time : 37.7566 secs

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(c) 1993 - 2004 Compugen Ltd.
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US-09-919-901-33
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; LENGTH: 2201 ; TYPE: PRT ; ORGANISM: Hepatitis US-09-539-601-6

C virus

Length 2201;

SOFTWARE: PatentIn Ver. SEQ ID NO 6

APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture
FILE REFERENCE: all sequences
CURRENT APPLICATION MUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION MUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 199-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1

System

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ALIGNMENTS

RESULT 1 US-09-539-601-6

Sequence 6, Application US/09539601C Patent No. 6630343
GENERAL INFORMATION:

밁 δ 뮍 Ş 밁 Ś 片 á 뮹 á 밁 Query Match Best Local S Matches 366 301 245 185 125 121 361 241 181 65 61 u Similarity GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR PPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN VQMAFMKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA GDIILGLPVSARRGREIHLGPADSLEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDRN VQMALMKLAALTGTYVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKVITWGADTAAC ILLTCAIHPELIFTITKILLAILGPLMVLQAGITKVPYFVRAHGLIRACMLVRKVAGGHY QVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQA PPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS Conservative 95.0%; Score 1951; DB 4; 93.1%; Pred. No. 8.8e-187; tive 14; Mismatches 13; 393 Indels 0; Gaps 184 180 124 64 364 360 300 244 240 60 304

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APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 3010
TYPE: PRT
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TITLE OF INVENTION: Hepathtis C Virus Cell Culture
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 2201
TYPE: PRT
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Best Local S
Matches 366
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Pred. No. 8.8e-187;
14; Mismatches 13;
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TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-539-601-21
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US-09-539-601-21
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Best Local Similarity 93.1
Matches 366; Conservative
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SEQ ID NO 21
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TITLE OF INVENTION: Hepatitis C Virus Cell
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
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Pred. No. 1.4e-186;
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Pred. No. 1.4e-186;
.4; Mismatches 13;
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APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture Sys
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 3010
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-539-601-27
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US-09-539-601-27
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GENERAL INFORMATION:
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Local Similarity 93.1%;
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GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
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                                                                  PPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPS
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k; Pred. No. 1.4e-186;
14; Mismatches 13;
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RESULT 6 US-09-263-933-4

Sequence 4, Application US/09263933 Patent No. 6280940

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APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/63,933
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1999-02-08
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1692
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; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-4
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US-09-919-901-4
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                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09919901
Patent No. 6599738
GENERAL INFORMATION:
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Robert
APPLICANT: Patick, Amy K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 4
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Best Local
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nilarity 92.9%;
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Pred. No. 1.9e-186;
l3; Mismatches 15;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN USE IN US/09/263,933
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
INDUSTRIES POSED ID NOS: 33
SOFTWARE: PATENT OF SEQ ID NOS: 33
SOFTWARE: PATENT OF SEQ ID NOS: 33
SOFTWARE: PATENT OF SEQ ID NOS: 33
SOFTWARE: PATENT OF SEQ ID NOS: 33
SOFTWARE: PATENT ORGANISM: Artificial Sequence
US-09-263-933-2
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US-09-263-933-2
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 365; Conserv
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Best Local :
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ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: :
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ILLTCAVHPELIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY 120
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                                                                                                                                                     94.8%; Score 1946; DB 3; Length 2307; ilarity 92.9%; Pred. No. 3e-186; Conservative 13; Mismatches 15; Indels 0
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APPLICANT: POTTS, KATEN E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/129,811

PRIOR APPLICATION NUMBER: 09/129,811

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOSTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 2307

TYPE: PRT

ORGANISM: Artificial Sequence
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US-09-919-901-2
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Patent No. 6599738
GENERAL INFORMATION:
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Best Local
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                 QVEGEVQVVSTATQSFLATCVMGVCWTVFHGAGSKTLAGFKGFITQMYTNVDQDLVGWQA
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                                                                    GDIILGLEVSARRGKEILLGEADSLEGRGWRLLAFITAYSQQTRGLLGCIITSLTGRDKN
                                                                                           GDIISGLFVSARRGREILLGPADNFEGOGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
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QVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGFKGFITQMYTNVDQDLVGWQA
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APPLICANT: BATTENSCHLAGER, Ralf FW
APPLICANT: BATTENSCHLAGER, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture Sys
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
LENGTH: 3010
TYPE: PRT
ORGANISM: Hepatitis C virus
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                                                                                                                  RESULT 11
US-09-263-933-11
; Sequence 11, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
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Best Local Similarity 92.9%;
Matches 365; Conservative 1
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APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
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%; Pred. No. 7.1e-186;
14; Mismatches 14; Indels
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; LENGTH: 1692
TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-11
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CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
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GHAVGIFRAAVCTRGVAKAVDFIFVESMETTMR 393
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                                                                           QVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGFKGF1TQMYTNVDQDLVGWQA
                                                                                                                                       QVEGEVQVVSTATQSFLATCVNGVCWTVFHGAGSKTLAGFKGFITQMYTNVDQDLVGWQA 300
                                                                                                                                                                                               GDIISGLPVSARRGREILLGPADNFEGGGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN
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                                                            PPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSAGGPLLCPS
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92.6%; Pred. No. 3.8e-186;
Pive 14: Mismatches 15;
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RESULT 12
US-09-919-901-11
; Sequence 11, Application US/09919901
; Sequence 11, Application US/09919901
; Patent No. 6599728
; Patent No. 6599728
; PAPLICANT: Potte, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Pattak, Amy K.
; APPLICANT: Pattak, Amy K.
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 3
; SOFTMARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1692
; OTHER INFORMATION: :
; OTHER INFORMATION: :
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APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR TITLE OF INVENTION: OF INHIBITORS OF THE HEP FILE REFERENCE: 0125-00054, US/09/263,933; CURRENT APPLICATION NUMBER: US/09/263,933; CURRENT FILING DATE: 1999-03-08

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 2307

TYPE: PRT

ORGANISM: Artificial Sequence
US-09-263-933-9
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US-09-263-933-9
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Patent No. 6280940
GENERAL INFORMATION:
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Sequence 9, Application US/09919901

| Sequence 10, Application US/09919901
| Patent No. 6599738
| GENERAL INFORMATION:
| APPLICANT: Potts, Karen E. APPLICANT: Potts, Amy K. APPLICANT: Potts, Amy K. APPLICANT: Patick, Amy K. APPLICANT: Patick, Amy K. APPLICANT: Patick, Amy K. APPLICANT: OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE FILE REFERENCE: 0125-0005A CURRENT APPLICATION NUMBER: US/09/919,901
| CURRENT FILING DATE: 2001-08-02 PRIOR APPLICATION NUMBER: 09/263,933 PRIOR APPLICATION NUMBER: 09/263,933 PRIOR FILING DATE: 1999-02-08 PRIOR FILING DATE: 1999-02-08 PRIOR FILING DATE: 1998-08-05 NUMBER OF SEQ ID NOS: 33
| SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 9 LENGTH: 2307
| TYPE: PRT ORGANISM: Artificial Sequence FEATURE: Pating Date: 1918-08-05 PATITIFE: PATICAL SEQUENCE
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GHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 393
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Pred. No. 6e-186;
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GHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 577

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Sequence 18, Application US/09263933

Patent No. 6280940

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Potts, Karen E.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHEITORS OF THE HEBATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/263,933

CURRENT APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION NUMBER: 09/129,611

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Search completed: May 6, 2004, 09:39:02 Job time : 16.4246 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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181 GDIISGLPVSARRGREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKN

121 VQMAFWKLAALTGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC 180

VOMAFMKLAALITGTYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAAC

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ALIGNMENTS

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NUMBER OF SEQ ID NOS: 21
SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 393
TYPE: PRT
ORGANISM: HCV
US-10-017-736-11
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US-10-017-736-11
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                                                                                                                                                                                           Query Match 100.0%; Score 2053; DB 13; Length 393; Best Local Similarity 100.0%; Pred. No. 2.2e-197; Matches 393; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Protease
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
PRIOR FILING DATE: 2000-12-15
                                 61 ILLTCAVHPELIFDITXLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY 120
  13
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                                                                                             1 MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
  ILLTCAVHPBLIFDITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHY 120
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Sequence 11, Application US/10650585
Publication No. US20040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Pr.
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING.DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 11
LENGTH: 393
TYPE: PRT
RESULT 3
US-10-017-736-2
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US-10-650-585-11
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US-10-650-585-11
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                                                                                GHAVGIFRAAVCTRGVAXAVDFIPVESMETTMR
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Pred. No. 2.2e-197;
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Best Local
                                          TYPE: PRT
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Sequence 2,

Application US/10017736

Query Match

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Score

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Sequence 2, Application US/10650585
Publication No. US20040077066A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
TITLE OF INVENTION: Purified Active HCV NS2/3 Pr.
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR PILING DATE: 2000-12-15
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GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim (Canada) Ltd.
ITITLE OF INVENTION: Purified Active HCV NS2/3 Pro-
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT ETLING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILLING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: HCV
US-10-017-736-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-10-650-585-2
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 409
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APPLICANT: Boebringer Ingelheim (Canada) Ltd.
ITITLE OF INVENTION: Purified Active HCV NS2/3 Pro
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/017,736
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
I NUMBER: OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 380
TYPE: PAT
ORGANISM: HCV
US-10-017-736-12
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                                   GREILLGPADNFEGOGWRLLAPITAYSOOTRGLLGCIITSLTGRDKNOVEGEVOVVSTAT
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TITLE OF INVENTION: Purified Active HCV NS2/3 Pro-
FILE REFERENCE: 13/082
CURRENT APPLICATION NUMBER: US/10/650,585
CURRENT FILING DATE: 2003-08-28
PRIOR APPLICATION NUMBER: US/10/017,736A
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/256,031
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 380
; Sequence 3, Application US/10029907

Publication No. US20020142350Al

; GENERAL INFORMATION:

; APPLICANT: BOEHRINGER INGELHEIM (C)
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; ORGANISM: HCV
US-10-650-585-12
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   INGELHEIM (CANADA)
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                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10309561
Publication No. US20030148348A1
GENERAL INFORMATION:
APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
TITLE OF INVENTION: HEPATITIS C VIRUS
FILE REFERENCE: 13/083
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       SEQ ID
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PRIOR APPLICATION NUMBER: US/10/029,907
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,857
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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                                                                                                                                                                                                                                       FILE REFERENCE: 13/083
CURRENT APPLICATION NUMBER: US/10/309,561
CURRENT FILING DATE: 2002-12-04
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OTHER INFORMATION: Xaa is Lys
NAME/KEY: VARIANT
LOCATION: 1489
OTHER INFORMATION: Xaa is Leu
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; Pred. No. 4.4e-186;
14; Mismatches 13;
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APPLICANT: De Francesco, Raffaele
APPLICANT: Migliaccio, Giovanni
APPLICANT: Migliaccio, Giovanni
APPLICANT: Migliaccio, Giovanni
ATITLE OF INVENTION: ENHANCED CELLS
FILE REFERENCE: ITRO003P
CURRENT APPLICATION NUMBER: US/10/467,000
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: PCT/EP02/00526
PRIOR APPLICATION NUMBER: PCT/EP02/00526
PRIOR APPLICATION NUMBER: 00/263,479
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEO ID NOS: 13
NUMBER OF SEO ID NOS: 13
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, LOCATION: 1489
, OTHER INFORMATION: Xaa
US-10-309-561-3
                                                  ; ORGANISM: Con 1
US-10-467-000-1
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Query Match
Best Local Similarity
                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
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Best Local
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FEATURE:
NAME/KEY: VARIANT
LOCATION: 882
OTHER INFORMATION: Xaa i
                                                                                     TYPE: PRT
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Local Similarity 93.1%;
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14; Mismatches 13;
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Sequence 4, Application US/09919901

Publication No. US20030082518A1

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Pattick, Amy K.

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT FILING DATE: 2001-08-02

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR FILING DATE: 1999-02-08

PRIOR FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1999-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 1892

TYPE: PRT

ORGANISM: Artificial Sequence
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US-09-919-901-4
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                                                                                                                                                  Query Match 94.8%; Score 1946; DB 10; Best Local Similarity 92.9%; Pred. No. 9.7e-186; Matches 365; Conservative 13; Mismatches 15;
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                                                                                                                      MAASCGGAVFIGLALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAI
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Matches 365; Conserv
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APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: US/29/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTINI DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTINI Ver. 2.0
SEQ'ID NO 4
LENGTH: 1692
TYPE: PAT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
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RESULT 13
US-10-191-966-2
US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GEMERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patick, Amy K.
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PRIOR APPLICATION NUMBER: 09/23,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Pocts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
CURRENT FILING DATE: 2001-08-02
CURRENT FILING DATE: 2001-08-02
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Best Local :
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OTHER INFORMATION: :
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Pred. No. 1.5e-185;
3; Mismatches 15;
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Sequence 11. Application US/09919901

Publication No. US20030082518A1

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

APPLICANT: Jackson, Roberta L.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/09/919,901

CURRENT APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/263,933

PRIOR APPLICATION NUMBER: 09/263,933

SOFTWARE: PATENT 198-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIN Ver. 2.0

LENGTH: 1692
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TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/09/263,933
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2307
TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 11, Application US/1019166

Publication No. US20030175692A1

GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Potts, Karen E.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CEL.
TITLE OF INVENTION: OF INHISTORS OF THE HEPATITIS C V
FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/9/263,933

PRIOR APPLICATION NUMBER: US/9/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR FILING DATE: 1999-03-08

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 1692

TYPE: PRI
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; ORGANISM: Artificial Sequence
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Similarity 92.6%; Pred. No. 1.9e-185;
64; Conservative 14; Mismatches 15;
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                                         PPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSAGGPLLCPS
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SUMMARIES

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ALIGNMENTS

ABG32185 standard; protein; 380 AA.

ABG32185;

HCV protease NS2/3 truncation mutant 827-1206. 05-NOV-2002 (first entry)

HCV; enzyme; protease; NS2/3 (827-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.

Hepatitis C virus. Synthetic.

WO200248375-A2.

20-JUN-2002.

13-DEC-2001; 2001WO-CA001796.

15-DEC-2000; 2000US-0256031P.

(BOEH) BOEHRINGER INGELHEIM CANADA LTD.

Thibeault D,

Lamarre

'n

Maurice R,

Pilote L,

Pause ď

Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation. WPI; 2002-599511/64.

Claim 41; Page 60-61; 67pp; English.

RRESULT 1
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ID ABG3
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XX HCP The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal residue amino acid 810 to 906, or rhaving a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length NS2/3 protease. Also included are (1) a composition (C) comprising an isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a mutated sequence, where the protease is in a solution comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide

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ARESULT 2
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ID 32184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                      HCV; enzyme; protease; NS2/3 (815-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO;
chaotropic agent; mutant; mutein.
                                                                                                                  HCV protease NS2/3 truncation mutant 815-1206.
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                                                                                                                                                                                                                                                               ABG32184 standard;
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Pred. No. 1.5e-184;
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1 ALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIF

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Gaps

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DITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTG ALLTESPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIF

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The invention relates to an isolated polypeptide consisting of a full-
CC length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred
CC to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal
CC residue amino acid 810 to 906, or having a minimal amino acid sequence
CC from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length
CC (NS2/3) protease. Also included are (1) a composition (c) comprising a sufficient concentration of lauryldathylamine oxide (LDAO)
CC comprising a sufficient concentration of lauryldathylamine oxide (LDAO)
CC appearing as ABG32198; (3) protease; (2) a NS2/3 inhibitory peptide
CC chaotropic agent, refolding the protease in the presence of a
CC reducing agent, and LDAO in the presence of reduced concentration of the
CC chaotropic agent or a polar additive; (4) producing (M1) an active NS2/3
CC protease; involving includating the isolated protease by contacting it with a
CC reducing agent or a polar additive; (4) producing (M2) an active NS2/3
CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3
CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3
CC protease; (5) measuring (M3) the auto-cleavage activity of NS2/3
CC protease; (6) screening a potential inhibitor of auto-cleavage activity of an activation of a potential inhibitor of auto-cleavage activity of an activation of a potential inhibitor of auto-cleavage activity of an active NS2/3 protease, cleavage products or their fragments. The protease in a consense of an active NS2/3 protease, cleavage products or their fragments of the presence of an active NS2/3 protease, cleavage products or their fragments of the presence of or absence of the potential inhibitor of auto-cleavage activity of an activity of an activity of an activity of an activity of an activity of an activity of an active NS2/3 protease in the presence of or a cleavage of the potential inhibitor of auto-cleavage activity of an activity of an activity of an activity of an activity of an activity of a
  Query Match
Best Local Similarity
Matches 380; Conserv
                                                                                       Sequence 393 AA;
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Synthetic.
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ilarity 100.0%;
Conservative 0
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Score 1987; DB 5;
Pred. No. 1.6e-184;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCV; enzyme; protease; NS2/3 (810-1206); hepatitis C virus infection; chronic liver disease; cirrhosis; end-stage liver disease; virucide; hepatotropic; antiinflammatory; lauryldiethylamine oxide; LDAO; chaotropic agent; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
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The invention relates to an isolated polypeptide consisting of a full-length HCV (hepatitis C virus) non-structural (NS)2/3 protease (referred to also as NS2/3 (810-1206)), or its truncation, having as its N-terminal residue amino acid 810 to 906, or having a minimal amino acid sequence from residues 904 to 1206 of hepatitis C virus (HCV) 1b-40 full-length NS2/3 protease. Also included are (1) a composition (C) comprising an isolated HCV NS2/3 protease selected from full length NS2/3 protease, or its truncation or a mutated sequence, where the protease is in a solution comprising a sufficient concentration of lauryldiethylamine oxide (LDAO) to prevent auto-cleavage of the protease; (2) a NS2/3 inhibitory peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV protease NS2/3 (810-1206).
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                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptide for screening inhibitors of non-structural proteases useful as therapeutic agents against hepatitis C virus, comprises full length non-structural protease, or its truncation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-2000; 2000US-0256031P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200248375-A2
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                                                                                                                                                                                                                                                                                                                                     Claim 42; Fig 1B; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 409
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16-OCT-2003 14-NOV-1996

(revised)
(first entry)

Partial HCV

non-structural polyprotein.

proteinase; hepatitis C virus; identification; cleavage.

screening; inhibitor; proteolytic,

AAR82694;

AAR82694 standard;

protein; 3010 AA.

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CC appearing as ABG32198; (3) producing (M1) a refolded, inactive HCV NS2/3 CC protease, involving isolating the protease in the presence of a cc chaotropic agent, refolding the isolated protease by contacting it with a CC reducing agent, and LDAO in the presence of reduced concentration of the CC chaotropic agent or a polar additive; (4) producing (M2) an active NS2/3 cc containing an activation detergent to induce auto-cleavage of the NS2/3 cc protease; (5) measuring (M3) the auto-cleavage activity of NS2/3 cc protease; involving incubating the active NS2/3 protease and produce cc cleavage products or their fragments, and measuring the presence or sensitive not their fragments, and measuring the produce of the NS2/3 protease, cleavage products or their fragments, and measuring the presence of cc active NS2/3 protease, involving carrying out M3 in the presence of, or active NS2/3 protease, cleavage products or their fragments of the presence of, or active NS2/3 protease, on the protease, cleavage products or their fragments. The protease is cuseful for detailed biochemical characterisation of the enzymes and in the development of in vitro assays for screening novel inhibitors of the enzymes which causes chronic liver disease, cirrhosis and end-stage created represents the NS2/3 (B10-1206) protein, which has a C-terminal errent-vivilin tag.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIF
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                                                                                                                                                                                                                                                                                                                                                                                           DITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTG 137
                    RGVAKAVDFIPVESMETTMR
                                                                                                    SSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCT 360
                                                                                                                                                                             OSFLATCVNGVCWTVFHGAGSKTLAGFKGFITQMYTNVDQDLVGWQAFFGARSMTFCTCG 300
                                                                                                                                                                                                                                 GREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTAT
    RGVAKAVDFI PVESMETTMR
                                                                             SSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCT
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    397
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07-FEB-1992; 18-SEP-1992; 04-DEC-1992; (KAEN/) 05-FEB-1993; JP07184648-A Protein Protein Hepatitis C) KAENNO K.) SUMITOMO METAL :) SOYAKU GIJUTSU ! 92JP-00022657. 92JP-00249240. 92JP-00325303. 93JP-00018854 /note= 992. .1 Location/Qualifiers 898. .1233 e= "partial proteinase;
.1907 IND LTD. "partial proteinase; see AAR82692"

N-PSDB; WPI; 1995-287962/38

KENKYUSHO

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An HCV V proteinase active and can be used to substance - which has activity as screen for proteinase inhibitors. an

Disclosure; Page 39-48; 52pp; Japanese.

The present sequence is a partial Hepatitis C Virus (HCV) polyprotein from the non-structral region. Partial proteinase sequences (AAR82692-93) are contained within this sequence. The proteinases can be used as anti-HCV agents. They can also be used to screen cpds. for their ability to inhibit their proteolytic activity. In this way proteinase inhibitors can be identified. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 3010 AA; Length 3010;

Query Match Best Local S Matches 357 al Similarity 357; Conserv Conservative 95.7%; Scu 94.2%; Pro-mative 12; Score 1902; DB 2; Pred. No. 5.3e-175; 2; Mismatches 10; Indels 0

밁 Ś Ś 뮍 Ś В 밁 Ş Ş 밁 S 밁 Ş 1068 1128 1008 362 302 242 182 948 122 888 828 62 N GVAKAVDFIPVESMETTMR 380 SDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTR SFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGS KEILIGPADSFGEQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQ REILLGPADNFEGOGWRLLAPITAYSOCTRGLLGCIITSLTGRDKNOVEGEVOVVSTATO YVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRG LLTLSFYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIFD SDLYLVTRHADVVPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPSGHVVGIFRAAVCTR YVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKLITWGADTAACGDIISGLPVSARRG ITKLLLAILGPLMVLQAGITRVPYFVRAQGLIRACMLVRKVAGGHYVQMAFMKLAALTGT ITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGT LITLSPYYKVFLARLIWMLQYFITRAEAHLQVWVPPLNVRGGRDAIILLTCAVHPELIFD 301 361 241 1007 181 947 887 61

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> DT C16-C
> DT This protein from HCV (hepatitis C virus) (encoded by AAQ80498) is cleaved between amino acids 2419 and 2420, by a new serine protease, contg. the sequence of AAR6821. The proteinase is purified as a fused product with the dihydrofolate reductase protein by using a methotrexate column. It can be used for the development of an inhibitor for HCV proteinase. (Updated on 16-OCT-2003 to standardise OS field) Disclosure; New HCV-originated proteinase active substance - used for site-specific cleavage by an intermolecular reaction and the purification thereof. WPI; 1995-032330/05. N-PSDB; AAQ80498. (KAEN/) 06-MAY-1993; Hepatitis C HCV protein 16-OCT-2003 16-OCT-1995 AAR68622 standard; protein; 15-NOV-1994 JP06315377-A Cleavage-site) KAENNO K.) SUMITOMO METAL) SOYAKU GIJUTSU Page 10-19; 23pp; Japanese. virus; Virus cleavable with new serine proteinase serine; cleavage; (first en 93JP-00105666 Location/Qualifiers 2419. .2420 /note= "Serine protease entry) IND IND LTD. KENKYUSHO 3010 쯪 cleavage C virus; HCV

Ś Query Match Best Local S Matches 356 356; 2 LLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIFD Similarity Conservative 95.5%; 12; Score Pred. Mismatches 1897; No. 1. DB 2; Length 3010; Indels 0 Gaps

0

Sequence 3010 AA;

δ 멼 B Ś 밁 Ś Ś 맑 밁 1068 1008 948 122 888 828 62 SDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTR SFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGS REILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQ YVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRG ITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGT SFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPCTCGS KEILLGPADSFGEQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQ YVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKLITWGADTAACGDIISGLPVSARRG LLTLSPYYKVFLARLIWWLQYFITRAEAHLQVWVPPLNVRGGRDAIILLTCAVHPELIFD ITKLLLPILGPLMVLQAGITRVPYFVRAQGLIRACMLVRKVAGGHYVQMAFMKLAALTGT 361 301 1067 1007 121 181 887 241 947

RESULT

1188

GVAKAVDFIPVESMETTMR

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         92JP-00249241
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Best Local
                                                                                         Misc-difference 81.
                                                                                                                                  Key
Misc-difference
                                                                                                                                                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                                                                       Recombinant hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ81559 encodes AAR68864 hepatitis C virus (HCV) RNA helicase. was used in the construction of an expression vector, which was transform a baculovirus host. The transformed baculovirus could used for the recombinant prodn. of HCV RNA helicase
                                            Duplication
                                                                                                                                                                                                                                          Hepatitis; HCV; virus; screening; antiviral drugs
                                                                                                                                                                                                                                                                                                                                    21-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                              AAR40223;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAR40223 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1-4; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of hepatitis C virus helicase gene in baculovirus - useful for large scale prodn. of RNA helicase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDLYLVTRHADVVPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPSGHVVGIFRAAVCTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITKLLLA LIGPLMVLQAGITR VPYFVRAQGLIRACMLVRKVAGGHYVQMA FMKLAALTGT
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                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                    Location/Qualifiers
528. .768
/note= "Duplication of 241 amino acids at start of
protein sequence."
                                                                  /note=
                                                                                                            note=
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93.9%; Pred. No. 2e-174;
tive 12; Mismatches 1
                                                                  "Nucleotide sequence encodes another Gly"
                                                                                                            "UUA encodes Ile."
                                                                                                                                                                                                                                                                                                                                                                                                                         768
                                                                                                                                                                                                                                                                                       genomic protein.
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RESULT 8
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ID ABG3
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AC ABG3
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DT 21-(
XX
DE Hep;
XX
KW Sel
KW Sel
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    Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor; cell culture replication; NS2/3; NS3/4; NS3; NS5B; mutant; mutein.
                               Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B mutant #10.
                                                      21-OCT-2002
                                                                                            ABG30601 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein is useful in the screening of HCV-specific antiviral drugs, HCV cDNA was cloned from plasma. Plasmids pSR3241 and pSR2541 were prepared using the cDNA and plasmid pSR3241 was used to transform a COS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 4-6; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus genomic RNA, cDNA and polypeptide - used hepatitis C virus-specific antivirus drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-277474/35.
N-PSDB; AAQ48215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                    RGVAKAVDFIPVESMETTMR 380
                                                                                                                                                                                               SSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCT 360
                                                                                                                                                                                                                                                                                                                                                   DITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTG
                                                                                                                                                                                                                                                                                                                                                                             ALLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIF
                                                                                                                                                                               SSDLYLVTRHADVIPVRRRGDTRGSLLSPRPISYLKGSSGGPLLCPSGHVVGIFRAAVCT
                                                                                                                                                                                                                                                                       GREILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTAT
                                                                                                                                                                                                                                                                                                            TYVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARR
                                                                                                                                                                                                                                                                                                                                       DITKLLLSILGPLMVLQASLIRVPYFVRAQGLIRACMLVRKAAGGHYVQMAFVKLAALTG
                                                                                                                                           RGVAKAVDFIPVESMETTMR
                                                                                                                                                                                                                     QSFLATCVNGACWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCG
                                                                                                                                                                                                                                        QSFLATCVNGVCWTVFHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCG
                                                                                                                                                                                                                                                          GKEILLGPADSFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTAT
                                                                                                                                                                                                                                                                                                 TYVYDHLTPLQDWAHVGLRDLAVAVEPVVFSAMETKVITWGADTAACGDIISGLPVSARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            768 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                    (first entry)
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                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                               95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 1888; DB
; Pred. No. 1.8e-
13; Mismatches
                                                                                           2201
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1.8e-174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 768;
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Дb Ś В 8 B Ś 밁 Ş 맑 8 밁

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The invention describes a self-replicating hepatitis C virus (HCV) CC polynucleotide molecule comprising a 5'-non translated region (NTR), CC where guanine at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein; and a 3'-NTR region. The self-creplicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating contential inhibitors of HCV replication. The HCV RNA molecule is also useful for efficiently establishing cell culture replication. The self-creplicating polynucleotide molecule contains a 5'-NTR, where G at position 1 is substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the CC existing systems comprising a self-replicating HCV RNA molecule that, in CC conjunction with mutations in the HCV non-structural region, such as the CC (12042) C/R mutations, transduces and/or replicates with greater CC efficiency. This amino acid sequence represents a mutant of the hepatitis CC virus replicate NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS2/3, protease complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note: This sequence does not appear in the specification but has been created from the wild type sequence shown in ABG30580 using information given in two claims of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 354; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2201 AA;
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Synthetic.
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                                                                                                                                                                                                                          YVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRG
                                                                                                      REILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQ
                                                                                                                                                                                                                                                                                                                                                 ITKLLLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGT
                                                        REIHLGPADSLEGOGWRLLAPITAYSOOTRGLLGCIITSLTGRDRNOVEGEVQVVSTATO
                                                                                                                                                                                         YVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKVITWGADTAACGDIILGLPVSARRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 1887; DB 5;
; Pred. No. 9.9e-174;
13; Mismatches 12;
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The invention describes a self-replicating hepatitis C virus (HCV) polynucleotide molecule comprising a 5'-non translated region (NTR), where guanine at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein, and a 3'-NTR region. The self-control of the first polyprotein, and a 3'-NTR region. The self-control inhibitors of HCV replication. The HCV RNA molecule is also potential inhibitors of HCV replication. The HCV RNA molecule is also consisted for efficiently establishing cell culture replication. The self-control for efficiently establishing cell culture replication. The self-consisting polynucleotide molecule contains a 5'-NTR, where G at conjunction is substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the conjunction with mutations in the HCV non-structural region, such as the conjunction with molecule sand/or replicates with greater cefficiency. This amino acid sequence represents a mutant of the hepatitis complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note: C virus replicates NS3 and RNA-dependent RNA polymerase NS5B. Note: C this sequence does not appear in the specification but has been created the wild type sequence shown in ABG30580 using information given in the claims of the invention
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New self-replicating RNA molecules from Hepatitis C virus (HCV), possess enhanced transduction or replication efficiency, useful evaluating potential inhibitors of HCV replication.

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ABG30600 ID ABG30 ABG30 ABG30 ABG30 ABG30 ABG30 XX ABG30 XX ABG30 XX Self-KW Self-KW Cell SX KW Cell SYNCH SY KW Cell SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SYNCH SY
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Best Local (
                                                                                                                        Self-replicating; hepatitis C virus; HCV; cell culture replication; NS2/3; NS3/4; NS
                                                                                                                                                                                                             Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B #1.
            WO200252015-A2
                                                                  Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGS
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; Pred. No. 9.9e-174;
13; Mismatches 12;
                                                                                                                        V; HCV replication inhibitor;
NS3; NS5B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a self-replicating hepatitis C virus (HCV) polynucleotide molecule comprising a 5'-non translated region (NTR), where guanine at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein; and a 3'-NTR region. The self-replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating potential inhibitors of HCV replication. The HCV RNA molecule is also useful for efficiently establishing cell culture replication. The self-replicating polynucleotide molecule contains a 5'-NTR, where G at position 1 is substituted for A, and therefore provides an alternative to existing systems comprising a self-replicating HCV RNA molecule that, in conjunction with mutations in the HCV non-structural region, such as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G(2042)C/R mutations, transduces and/or replicates with greater efficiency. This amino acid sequence is encoded by the hepatitis C virus replicon APGK12 and contains the viral protease NS2/3, protease complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 49-58; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New self-replicating RNA molecules from Hepatitis C virus (HCV), which possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kukolj G,
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DB; ABK88573.
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                GVAKAVDFIPVESMETTMR
                                                                                                                                                                                                                           REILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDXNQVEGEVQVVSTATQ
                                                                                                                                                                                                                                                                                                   YVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRG
                                                                                                                                                                                                                                                                                                                                                                                                                                          LLTLSPYYKVLLARLIWMLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIFD
                                                                                        SDLYLVTRHADVI PVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGI FRAAVCTR
                                                                                                                                    SFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGS
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GVAKAVDEVEVSMETTMR
                                                                  SDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTR
                                                                                                                                                                    SELATCVNGVCWTVEHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGS
                                                                                                                                                                                                         REIHLGPADSLEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pause A;
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93.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1887; DB 5;
; Pred. No. 9.9e-174;
13; Mismatches 12;
                               380
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standard;

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CC polynucleotide molecule comprising a 5'-non translated region (NTR),

CC where guanine at position 1 is substituted for adenine, a HCV polyprotein

CC region coding for a HCV polyprotein, and a 3'-NUR region. The self-

CC replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating

CC otential inhibitors of HCV replication. The HCV RNA molecule is also

CC useful for efficiently establishing cell culture replication. The self-

CC replicating polynucleotide molecule contains a 5'-NUR, where G at

CC position 1 is substituted for A, and therefore provides an alternative to

CC existing systems comprising a self-replicating HCV RNA molecule that, in

CC conjunction with mutations in the HCV non-structural region, such as the

CC (2042)C/R mutations, transduces and/or replicates with greater

CC efficiency. This amino acid sequence represents a mutant of the hepatitis

CC virus replicon APGK12 and contains the viral protease NSC3, protease

CC complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note:

CC complex NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B. Note:

CC this sequence does not appear in the specification but has been created

CC the claims of the invention
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                                                                                                                                         Query Match
Best Local :
                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New self-replicating RNA molecules from Hepatitis C virus (HCV), wh possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page; 140pp; English
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                                                                                                                                                                                           Sequence 2201 AA;
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                                                                                                                                         Similarity
                                                           LLTLSPYYKVLLARLIWWLQYLITRVEAHLQVWIPPLNVRGGRDAIILLTCAVHPELIFD 61
ITKILLAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGT 121
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                                                                                                                                           95.0%;
93.4%;
                                                                                                                            13;
                                                                                                                            Score 1887; DB 5;
Pred. No. 9.9e-174;
.3; Mismatches 12;
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                                                                                                                                                          Length 2201;
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                                                                                                                                                                                                                                                                                                                                         New self-replicating RNA molecules from Hepatitis C virus (HCV), which possess enhanced transduction or replication efficiency, useful for evaluating potential inhibitors of HCV replication.
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N-PSDB; ABK88574.
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NS3; NS5B; mutant; mutein.
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The invention describes a self-replicating hepatitis C virus (HCV) polynucleotide molecule comprising a 5'-non translated region (NTR), where guanine at position 1 is substituted for adenine, a HCV polyprotein region coding for a HCV polyprotein; and a 3'-NTR region. The self-replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating potential inhibitors of HCV replication. The HCV RNA molecule is also useful for efficiently establishing cell culture replication. The self-replication polynucleotide molecule contains a 5'-NTR, where G at position 1 is substituted for A, and therefore provides an alternative to existing systems comprising a self-replicating HCV RNA molecule that, in

Disclosure; Page 59-69; 140pp; English.

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Best Local
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                            Kukolj G,
                                                                                                                                  22-DEC-2000; 2000US-0257857P
                                                                                                                                                                                                                                             04-JUL-2002
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                                                                                  (BOEH ) BOEHRINGER INGELHEIM CANADA
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                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG30580 standard;
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93.4%;
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Pred. No. 9.9e-174;
.3; Mismatches 12;
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DR WPI; 2002-575382/61.

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New self-replicating RNA molecules from Hepatitis C virus (HCV), which PT possess enhanced transduction or replication efficiency, useful for PT evaluating potential inhibitors of HCV replication.

XX

Disclosure; Page 69-74; 140pp; English.

XX

CC The invention describes a self-replicating hepatitis C virus (HCV) CC polynucleotide molecule comprising a 5'-non translated region (NTR), CC where guanine at position 1 is substituted for adenine, a HCV polyprotein coding for a HCV polyprotein; and a 3'-NTR region. The self-cc replicating Hepatitis C virus (HCV) RNA molecule is useful for evaluating CC useful for efficiently establishing cell culture replication. The self-cplicating polynucleotide molecule contains a 5'-NTR, where G at CC position 1 is substituted for A, and therefore provides an alternative to conjunction with mutations in the HCV non-structural region, such as the CC conjunction with mutations in the HCV non-structural region, such as the CC (2042)C/R mutations, transduces and/or replicates with greater cC efficiency. This amino acid sequence is encoded by the hepatitis C virus (CC NS3/4, helicase NS3 and RNA-dependent RNA polymerase NS5B Sequence 2201 AA;

Ouery Match 95.0%; Score 1887; DB 5; Length 2201; Best Local Similarity 93.4%; Pred. NO. 9.9e-174; Matches 354; Conservative 13; Mismatches 12; Indels 0; Gaps 0; CV 2 LittsPyykyLlarRLIWMLOYLITRVEAHLOWMIPPLAVRGGRADAIILLTCAVHPELIFD 61
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             GVAKAVDFIPVESMETTMR
                                                                                                                             SFLATCVNGVCWTVFHGAGSKTLAGFKGPITQMYTNVDQDLVGWQAFPGARSMTPCTCGS
GVAKAVDFVPVESMETTMR
                                                      SDLYLVTRHADVIPVRRRGDSRGSILSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTR
                                                                                                                                                                                   REILLGPADNFEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQ
                                                                               SDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTR
                                                                                                            SFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGS
                                                                                                                                                                   REIHLGPADSLEGQGWRLLAPITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQ
                                                                                                                                                                                                                         YVYDHLTPLRDWAHAGLRDLAVAVEPVVFSDMETKVITWGADTAACGDIILGLPVSARRG
                                                                                                                                                                                                                                            YVYDHLTPLQDWAHAGLRDLAVAVEPVIFSDMEVKIITWGADTAACGDIISGLPVSARRG
                                                                                                                                                                                                                                                                                                    ITKLILAIFGPLMVLQAGITKVPYFVRAQGLIRACMLVRKAAGGHYVQMAFMKLAALTGT
                                                                                                                                                                                                                                                                                                                                       LITLSPHYKLFLARLIWMLQYFITRABAHLQVMIPPLNVRGGRDAVILLTCAIHPELIFT
                                                                                                                                                                                                                                                                                  ITKILLAILGPLMVLQAGITKVPYFVRAHGLIRACMLVRKVAGGHYVQMALMKLAALTGT
397
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RESULT 15
ABG30587

ABG30587 standard; protein; 2201 AA.

XX

AC ABG30587;

XX

DT 21-CCT-2002 (first entry)

XX

DE Hepatitis C virus NS2/3, NS3/4, NS3 and NS5B #7.

XX

XX

KW Self-replicating; hepatitis C virus; HCV; HCV replication inhibitor;

XX

XX

Cell culture replication; NS2/3; NS3/4; NS3; NS5B.

XX

CS Hepatitis C virus.
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